

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2002, 01:38:50 ; Search time 2103.63 Seconds
(without alignments)
12888.008 Million cell updates/sec

Title: US-09-715-962-1

Perfect score: 2523

Sequence: 1 atgcgcaagatatgacaag.....caatcacacaagtgtagtag 2523

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```
EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: gb_est1:*
11: gb_est2:*
12: gb_hic:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vit:*
21: em_gss_other:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198.6	7.9	740	11	BG818076 602779584
2	179.6	7.1	1101	13	AL063634 Drosophila
3	175.4	7.0	450	10	AL119755 DKF2P761C
4	147.4	5.8	566	10	AU206445 AU206445
5	139.6	5.5	572	11	BF530404 BF530404
6	123.2	4.9	393	10	AW158263 AW158263
7	122.8	4.9	859	11	BG423148 BG423148
8	116	4.6	398	10	AA036134 AA036134
9	115.6	4.6	611	11	X90542 X90542
10	112.4	4.5	512	10	AW049355 AW049355
11	110.8	4.4	492	11	X90543 X90543
12	103.4	4.1	445	11	BI037782 BI037782

13	100.6	4.0	665	11	BG820975
14	99.4	3.9	335	10	AL602784
15	99.4	3.9	459	10	AL042317
16	98	3.9	952	11	BG911698
17	96	3.8	418	10	BE702435
18	93.2	3.7	399	10	AA038839
19	93.2	3.7	918	11	BF529670
20	92.8	3.7	834	10	AL134060
21	92.2	3.7	869	10	AL539611
22	92	3.6	325	11	BF932595
23	91.6	3.6	386	11	D80024
24	88.8	3.5	329	11	BF932593
25	87.6	3.5	712	10	AU218430
26	81.6	3.2	624	10	AW960962
27	79	3.1	296	11	BF950810
28	75.2	3.0	604	11	BG819622
29	73.8	2.9	315	11	BG986345
30	72.2	2.9	330	10	BE654255
31	69.8	2.8	867	13	CNS02X44
32	69.6	2.8	704	11	BG773057
33	69.2	2.7	525	10	AW383370
34	68.8	2.7	443	11	BG987524
35	66.8	2.6	913	11	BF791371
36	65.2	2.6	191	11	BI039561
37	64.8	2.6	452	13	BH100127
38	64.8	2.6	599	13	BH100872
39	63.4	2.5	283	10	AA324303
40	63	2.5	1063	11	BF799281
41	62.6	2.5	483	10	AI119788
42	61.6	2.4	551	11	BF194073
43	61.2	2.4	619	10	AI404922
44	60.8	2.4	320	10	AW380854
45	60	2.4	303	10	AW380861

ALIGNMENTS

RESULT 1

LOCUS BG818076 740 bp mRNA EST 22-MAY-2001
DEFINITION 602779584F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4915244
5', mRNA sequence.
ACCESSION BG818076
VERSION BG818076.1 GI:14165663
KEYWORDS EST
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 740)

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: David N. Louis, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM10823 row: g column: 21

High quality sequence stop: 735.

Location/Qualifiers

1. 740

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4915244"

/clone_lib="NCI_CGAP_Brn67"

/tissue_type="anaplastic oligodendroglioma with lp/19q loss"

```
/lab_host="DH10B (T1 phage-resistant)"
/Note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      187 a   194 c   193 g   166 t
ORIGIN

Query Match
Best Local Similarity 7.9%; Score 198.6; DB 11; Length 740;
Matches 430; Conservative 0; Mismatches 294; Indels 25; Gaps 3;

QY 442 cgattcccaactattccgcaccatccatccgagccaggtgacacatcccaacgcgcac 501
D 1 CGTTTCCCACTTTCTCCGAAGCCACCCATCAGCCACACTCCACACACCTTACC CGGTG 60

QY 502 aagctgatgaagaattcggctgggtccgggtggccattctgcagcaggcgagagatc 561
D 1 AACTCTTTGAAAGTGGGGCTGGAAGAAGATTGCTACCATCCAGCAGCACCACCTGAGT 120

QY 562 ttatatcgaccctgaagctcgaagaatcgatgcagaggtggtggtgaaatcgta 621
D 1 TACATTCGACTCTGGAGCAGCTGGAGGAGCGAGTGAAGGAGGTGGAATTGAGATTACT 180

QY 622 actagacaatcttctatccgattcccaacagacgcgcgtgcgaatttgcgacgcagat 681
D 1 TTCCGCCAGAGTTCTCTCAGATCCAGCTGTGCCGCTCAAAAACCTGAAGCGCAGGAT 240

QY 682 gcacgcacatctgtgggactctctatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 741
D 1 GCCCGAATCATCGTGGGACTTTCTATGAGACTGAAGCGCCGAAAGTTTTTTTGTGAGTG 300

QY 742 tacaacacagcagctatgtgcccagctatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 801
D 1 TACAAGGAGCGCTCTTTTGGGAGAGAACTGCTGTCTCTCTCTCTCTCTCTCTCTCTCT 360

QY 802 aactggtacaggtggaatctgaaagcagagggcgcacactcactgttgaaacagatcga 861
D 1 AATGTTCAAGATCTACGACCCCTTC-----TATCAACTGCACAGTGGATGAGATGACT 414

QY 862 atagctgccgaagacatctgacacgaagcgcgtcctatgtggaatcagaacaatcagaca 921
D 1 GAGCGGTGGAGGCCACATCACAACCTGAGATTGCTGCTGATCTGCTGCTGCTGCTGCTG 474

QY 922 actatattccggaatgactgagagaattttgcacatgcactgactgagcgcctaatcag 981
D 1 AGCATTTTCAACATGACATCCAGGAATTTGTGGAGAAACTTAACCAAGCGACT----- 527

QY 982 gaggggtacgacattacccagcgcgtatccgagggatcagagggcgcacactcgc 1041
D 1 -----GAAAGACACCTTGAGAGACAGAGGCTTCCAGAGGCGACCGCTGGCC 576

QY 1042 tacgatgcagtgagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1101
D 1 TATGATGCCATCTGGGCTTGGCACTGGCCCTGAACAGACATCTGGAGGAGCGCGGCTT 636

QY 1102 ggaagaatactctgagggattttacctatatacgcagagagagattgccgatgaaatctac 1161
D 1 CTGCTGTGCGC-CTGGAGGAGCTTCAACTACAAACACAGACCATTAACCGACCAATCTCT 695

QY 1162 gctgccaatgaactccacacaatttctggg 1190
D 1 CCGGCAATGAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 724

RESULT 2
CNS000BA 1101 bp DNA GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BR0101C07 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL063634
```

```
VERSION AL063634.1 GI:4938682
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
pterygota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
Location/Qualifiers
source 1..1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR01C07"
/note="end : TET3"
BASE COUNT 303 a 206 c 209 g 361 t 22 others
ORIGIN

Query Match 7.1%; Score 179.6; DB 13; Length 1101;
Best Local Similarity 99.0%; Pred. No. 2.4e-40;
Matches 190; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2332 cagaagaggaatttcagctcctgcacagcgtctgtagcgagcgagcgagcgaag 2391
D 1 cagaagaggaatttcagctcctgcacagcgtctgtagcgagcgagcgagcgaag 2391

QY 2392 ggcacagaactgaattgtgcaacaggtgtcgctccgcgcgcgttgcacaaacttcgag 2451
D 1 ggcacagaactgaattgtgcaacaggtgtcgctccgcgcgcgttgcacaaacttcgag 2451

QY 2452 cccgttcctccatcaactcatcagcacatgcccacgcgcgcgcgcgcgcgcgcgcgcgc 2511
D 1 cccgttcctccatcaactcatcagcacatgcccacgcgcgcgcgcgcgcgcgcgcgcgc 2511

QY 2512 caagtgagtag 2523
D 1 caagtgagtag 2523

QY 2523 caagtgagtag 2523
D 1 caagtgagtag 2523

QY 2528 caagtgagtag 539
D 1 caagtgagtag 539

RESULT 3
AL119755 450 bp mRNA EST 25-FEB-2000
LOCUS Dfz7p761C0724_r1 761 (synonym: hamy2) Homo sapiens cDNA clone
DEFINITION Dfz7p761C0724 5', mRNA sequence.
ACCESSION AL119755
VERSION AL119755
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 450)
```

AU206445
AU206445.1 GI:14839613
EST.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditia; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
1 (bases 1 to 566)
Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
and Sugano, S.

Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

```

Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1. .566
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk864d02"
/clone_lib="unpublished oligo-capped cDNA library, stage

```

```

Li
/sex="Hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
154 a 116 c 130 g 165 t 1 others

```

ch 5.8%; Score 147.4; DB 10; Length 566;

1; Gaps 3; Indels 201; Mismatches 0; Conservative 57.9%; Pred. No. 3.9e-31; Score 147.4; DB 10; Mengchi 300; 3.8%;

g g g c g t g c c g g g g c c c g a t g a a c t g c a c a t g c g c g g c a t c t t t c g a t --- a g c c 138
| | | | | | | | | | | | | | | | | | | |
t g t g s g c t t c g c c g a g c g g t c a c c t t t c a c a t c g g t g g c a c g t t t c c g a t g g a a t c t 136

[illegible]

atgtcaacaagcagccgaattctgctgcgggcttcaagctcatctgcacagcaacgac 258
||||| | | | | | | | | | | | | |
ttgtgcaatagtcgatttagatatctaccttggttagctacttaatatgactaatctaac 256

318 **tcgcagctgagcccggtttggcgccagcgtgatgacaactctgctctataataaacg**
 319
 320 **ggcagctgcaacccagctcttgctatgcacaattatgattttctttataaccacct**
 321

GCAGTGCACCAAGCTTGTCTATGCAACAATTATATGATTTTCTTTATAAACCACT 316
aaagctgatgctgttgccagatgcagcaggtctgcaccactgtagccgaggtgcc 378

CGAGCTCATGCTTACAGGATGTAGTCCGTCAACTGTATTTGCTGAAGTCG 376
aaatgtgaatctaattgtctctgtacggggctcgagtcggtcttttcggatcgc 438

aaacattcccccaactattccagaccattccatcgccacgacgtgcacaatccaaagcgc 498
 ttagtctggaactatgctctgctcgaagggcctcagtcacgcgtgttttcgagatcgc 438
 ttt 436
 ttagtctggaactatgctctgctcgaagggcctcagtcacgcgtgttttcgagatcgc 436

aaagattcccaactctatccgcaccccatcactcgccacgtgcaaatccaacgcgc 498
||||| |||| | |||| | |||| | |||| | |||| | |||| | ||||
TGTGATCCCAACATGTTTCAGGACTCACCGCTCAGCGAATATGCAGAACCACCGGA 496

ccagctgataagaagaattcggctgtcccgggtgccattctgcagcgcgaggag 558
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
TTCACATAATCGAAAAAATCAAAATCGAAAAGATTTACTATTGTCGGTGTAGGAA 556

ctc 563
||
||
ttt 561

Qy	1805	catggcagaatctttgatccgcgtgcagcgttatctcgaaacattcccactcgaagatccag	1864
Db	61	TCTGGCAGATAGTGGACCCCTTACAGCGTTCTATTGAGGAATTTACCAAGAAGAACCTC	120
Qy	1865	tatctactactgatgatattaaaaatcgtccagagcttgagcattgtgaaagtcaacgca	1924
Db	121	GTGGTGACCTGSGATGTTCTC---ATACTCCCGACGTGGAACACTCAGTTCTCTCAAGA	177
Qy	1925	actccatgtgttggtcttggtatcagcgtctcaaggcgctaactcctgggtgtttggcctct	1984
Db	178	TGAACACATGGCTTGGTAGTATATGCGCTAAAGGGCTACTCTTTTTCGTTGGTATAT	237
Qy	1985	tttggcgtagagacgcgcctccattaaagtgaacacagatcaacgattcgcgttagtgag	2044
Db	238	TCTTGGCCTATGAGACCAAGAGTGTTTCACTGAGAAGATCAATGACCACCGTGTGTGG	297
Qy	2045	gcatgacatctataacgtggctgcctcttggctgataacagctccggtggcgatggtca	2104
Db	298	GGATGGCTATATACAATGTGGGTGTCCTTGGCTCATCACCCTCCAGTGACAAATGATCC	357
Qy	2105	ttgcacgcgaacaggacgcgtcctttgcttc	2136
Db	358	TCAGTAGCCAGCAGGACGCTTCCTTTGCATTC	389

```

RESULT 7
BG423148
LOCUS      602450359f1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4588791 5',
DEFINITION mRNA sequence.
ACCESSION  BG423148
VERSION     BG423148.1 GI:13329654
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  1 (bases 1 to 859)
            NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL
COMMENT    Contact: Robert Strausberg, Ph.D.

```

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLC1M321 row: e column: 16
High quality sequence stop: 729.

```

FEATURES
source
1. 859
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4588791"
/clone_lib="NIH_MGC_14"
/tissue_type="renal Cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: kidney; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
215 a 219 c 260 q 165 t
BASE COUNT

```

Query Match 4.98; Score 122.8; DB 11; Length 859;

[illegible]

RESULT 8
AA036134/c
LOCUS
DEFINITION
AA036134 398 bp mRNA 26-AUG-1996
mi75a09.r1 Soares mouse p3NMP19.5 Mus musculus cDNA clone
IMAGE:472408 5', mRNA sequence.
AA036134
AA036134.1 GI:1509324
EST.
house mouse.
Mus musculus.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 398)
Marra,M., Hillier,L., Allien,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,F., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE
The WashU-HMMI Mouse EST Project
JOURNAL
Unpublished (1996)
CONTACT: Marra M/Mouse EST Project
WASHU-HMMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

Fax: 314 286 1810
 Email: mousestewatson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:283152
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 371.
 Location/Qualifiers
 1. .398
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:472408"
 /clone_lib="Soares mouse p3NMF19.5"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Vector: pT73B (pharmacia) with a modified
 polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAAGTGAGCGCGCGCAATTTTTTTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldo. RNA was kindly provided by
 Dr. Minoru KO (Wayne State University)."
 100 a 91 c 118 q 89 t
 BASE COUNT

[illegible]

RESULT	9	
X90542/c		
LOCUS	X90542	611 bp mRNA
DEFINITION	HSGT545 Human Pgasparini Homo sapiens cDNA clone GT 545, mRNA sequence.	EST 20-MAY-1996
ACCESSION	X90542	
VERSION	X90542.1	GI:1296643
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 611) J. J. Roetto, A. Camaschella, C., De Sandre, G. and Gasparini, P. Toto, A., Rommens, J. M., Grifa, A., Lunardi, C., Carella, M., Huizenga Hereditary hemochromatosis: generation of a transcription map within a refined and extended map of the HLA class I region Genomics 31 (3), 319-326 (1996) 96435427 Contact: P. Gasparini Medical Genetics Service Hospital, I.R.C.C.S. 'CASA Soll. Sofferenza' Viale Cappuccini, 71013 San Giovanni Rotondo, Foggia, ITALY.	
FEATURES	Location/Qualifiers
source	1. 611 /organism="Homo sapiens" /db_xref="taxon:9606" /map="6p21.3" /clone="GT 545" /clone.lib="Human PGasparini"
BASE COUNT	159 a 150 c 174 g 126 t
ORIGIN	2 others

Query Match	4.68;	Score 115.6;	DB 11;	Length 611;
Best Local Similarity	51.08;	Pred. No. 5.8e-22;		
Matches 294;	Conservative 0;	Mismatches 281;	Indels 1;	Gaps 1;
Qy 1114	ctgagggaatttaactatacgcgacaagagagattgcccatgaaatctacgtcgccatgaac	1173		
Db 576	CGGAGGACTTCACTACACAACATAGACCATTACCGACCAAAATCTACCGGGCAATGAAC	517		
Qy 1174	tccacacaattttcgggtgtatcggggtgtgtggcattcagttcttcagggcgagtcgtatt	1233		
Db 516	TCTTCGTCTTTGAGGGTGTCTCTGGCCATGTGGTGTGTGATGTCACGGGTCTCGGATGG	457		
Qy 1234	gctettacacagatgcgaagatgatagacggcgaagtagcagaagaatttggtttactacgat	1293		
Db 456	CATGGACGCTTATCGGAGCAGCCCTCAGGGTGGCAGCTACAAGAAGATGGGCTACTATGAC	397		
Qy 1294	actcagttggataacctatcctcgtgtgtaatactgaacagtggaattggtggcgaagttcct	1353		
Db 396	AGCACCAGGATGATCTTCTCTGGTCCAAACACAGATAAATGGATTGGAGGTCGCCCCCA	337		
Qy 1354	caagatgcacaaattgtcaccccatgttctacgcaccgtgtccttgccattatttgbtgc	1413		
Db 336	GCTGACCAGACCCGTGTCATCAAAACATTCGCGTTCCTGTCAAGAAACTCTTTATCTCC	277		
Qy 1414	atgtgcacaatatccagtttggcattcttcgttccttcgcttgatcattcattaaata	1473		
Db 276	GTCACAGTTCCTCCAGCCTGGCAATTTGCTCTAGCTGTTGTGTGTCTGTCTTAAACATC	217		
Qy 1474	tggataagcatagaagagtaatacaatcctcgcatacccgctttgcaatacgcatacttta	1533		
Db 216	TACAACTCACATGTCCGTTATATCAGAACATCAGAGCCCAACCTGAACAACCTGACTGCT	157		
Qy 1534	ttgggtgcatacatgtctcaatatctgtcattcttacttgctggcgcatgcagcagctttgct	1593		
Db 156	GTGGGCTGCTTACTTGGCTTTTACGTGCTCTCTTCCCTCTGGGNGCTGATGGTTACCAAT	97		
Qy 1594	agccccgagggaatattccaaagatatgtcaagcgcggggttggtttactatcacccggtttt	1653		
Db 96	GGGAGGACCAAGTTTCCTTTCGTCTGCGCAGGCNCCCTC-TGGCTCCTGGGCGCTGGGCTTT	38		
Qy 1654	acactgatacagcgtgtctatgttcaagcaaggtctgg	1689		
Db 37	AGTCTGGGCTACGGTTCCTGTTCCATGTTTACCACCAAGATTTTCG	2		

RESULT 10	LOCUS	mRNA	EST	18-SEP-1999
AW049355/c	AW049355	512 bp		
	U1-M-RH1-ane-a-02-0-III s1	NTH	BMAP M S2	Mus musculus cDNA clone
	DEFINITION			

UI-M-BH1-ane-a-02-0-UI 3', mRNA sequence.

AW049355
VERSION
AW049355.1 GI:5909884
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
TITLE
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
available by the means that is soon to be determined. When NIH
determines the means for distribution of the BMAP cDNA clones, this
record will be updated accordingly when that means is determined.
Seq primer: M13 Forward
POLYA=No.

FEATURES

Location/Qualifiers

1..512
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="UI-M-BH1-ane-a-02-0-UI"
/clone_lib="NIH_BMAP_M_S2"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S2 library is a subtracted library derived from
NIH_BMAP_M_S1, which in turn is a subtracted library
derived from a mixture of normalized libraries from ten
regions of the mouse brain (cerebellum, brain stems,
olfactory bulbs, hypothalamus, cortex, amygdala, basal
ganglia, pineal gland, striatum, hippocampus). The driver
used for subtraction consisted of a pool of 5,000 clones
from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
obtained from non-normalized and normalized mouse brain
spinal cord libraries.
TAG_L1B=NIH_BMAP_M_S2
TAG_TISSUE=prefrontal-cortex
TAG_SEQ=GCCTCA"

BASE COUNT 121 a 132 c 133 g 126 t

Query Match 4.5%; Score 112.4; DB 10; Length 512;
Best Local Similarity 53.5%; Pred. No. 4.6e-21;
Matches 261; Conservative 0; Mismatches 221; Indels 6; Gaps 1;

QY 1898 agcttgagcatgtgaagtcacacgcaactccatggtggtggtctgtatagcggtctca 1957

DB 512 AGCTGGAGCAGTCGACGCTCCAGAAAGATGAATACATGCTCGGCATTTCTATGGTTACA 453

QY 1958 aggggctaactcgtgtgttggtccttttttggcgtagcagacgcgcctccattaaatga 2017

DB 452 AAGGGCTGCTGCTGCTGCTGGGAATCTTTCTGCTTATGAGACCAAAAGTGTGCCACTG 393

QY 2018 acaagatacaacattcgtgtatgtgggcatgagcatctatacattggtcgtctttggc 2077

DB 392 AAAAGATCAATGACCAACAGGGCGGTGGGATGCTATCTCAATGTTGCGGTCTGTGTC 333

QY 2078 tgataacagctccggtgggcatggttcattgcacgcaacagagcgcgtctcttgccttgg 2137
DB 332 TCATTACCGCTCCTGTCACCATGATCCTTTCCAGCCAGCAGCAGCGCTTCGCGCTTG 273
QY 2138 ttgctctagctgtgatattcttcttaagcatgctgctgtgatttggccaaaagg 2197
DB 272 CCTCTCTGGCCATTGTTCTCTCTCTACATTACTCTGGTGTGCTCTTTTGTGCTTAAGA 213
QY 2198 tcatcgaggttat-----acgtcatcccaagataagccgaatcgaatacaatcccg 2251
DB 212 TCGCAGGTTGATCACTCGAGGTGAATGCGAGTCTCTGAAGCACAGGACACAATGAACAACAG 153
QY 2252 attcagccatatcgaaagaggacgacgctctatcagaaacttgttaccgaaacagcgc 2311
DB 152 GATCATCCACCAACACATGAGGAGAGAGTCCCGACTGTTGGAGAGGAAACCGTG 93
QY 2312 aattgcaacgattataacacagaggaggaagaaagattcgactcctgcacagcgtctgg 2371
DB 92 AATTGGAAAAGATCATCGCCGAGAGAGAGGAGCGTGTCTCTGAACCTGCGCCATCAGCTCC 33
QY 2372 tggagcgg 2379
DB 32 AGTCTCGG 25

RESULT 11

X90543/c

LOCUS

DEFINITION X90543 492 bp mRNA EST 20-MAY-1996
HSGT546 Human PGasparini Homo sapiens cDNA clone GT 546, mRNA
sequence.

ACCESSION X90543

VERSION X90543.1 GI:1296644

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 492)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE
Tofaro,A., Rommens,J.M., Grifa,A., Lunardi,C., Carella,M., Huizenga
,J.J., Roetto,A., Camaschella,C., De Sandre,G. and Gasparini,P.
Hereditary hemochromatosis: generation of a transcription map
within a refined and extended map of the HLA class I region
Genomics 31 (3), 319-326 (1996)

JOURNAL 96435427

MEDLINE

COMMENT

Contact: P. Gasparini

Medical Genetics Service Hospital, I.R.C.C.S. 'CASA Soll.

Sofferenza'

Viale Cappuccini, 71013 San Giovanni Rotondo, Foggia, ITALY.

Location/Qualifiers

source

1..492

/organism="Homo sapiens"

/db_xref="taxon:9606"

/map="6p21.3"

/clone="GT 546"

/clone_lib="Human PGasparini"

BASE COUNT 113 a 138 c 113 g 125 t

ORIGIN

Query Match 4.4%; Score 110.8; DB 11; Length 492;

Best Local Similarity 55.5%; Pred. NO. 1.3e-20;

Matches 287; Conservative 0; Mismatches 205; Indels 25; Gaps 3;

QY 575 tagagatctcgagaatcgatgcagctgaggctggcgttgaaatcgtaactagacaatcat 634

DB 492 TGGACGACCTGGAGAACGAGTGAAGAGGCTTGAATTTGAGATTACTTTCCGCCAGAGTT 433

QY 635 ttctatcgatcccaacagacgcgcgtgcgaatttgcgacccagatgcacacatcatg 694

DB 432 TCTCTCAGATCCACCTGTGCCCCGTCACAAACCTGAAGCCCGCAGGATGCCCAATCATCG 373

QY 695 tgggactcttctatgtggtggccgacagaggtgctctgcgaaatgtacaaacagcgc 754

```
Db 372 TGGGACTTTCCTATGAGACTGAAGCCCGGA-AGTTTTTTTGTGAGGTGTACAAGGAGCGTC 314
QY 755 tatatgcccagctcatgtgtgtttttatttattgctggtgagagacaaactggtacgagg 814
Db 313 TCTTTGGGAAGTAGTACGTCTGCTCCTCATTTGGTGGTGTGCTGACAAATTGGT----- 258
QY 815 tgaatctgaagcagagggcctacactgactgacttgaacagagatgcgtaagtgcgcgaag 874
Db 259 TCAAGATCTACGACCCCTTCTATCACTGACAGTGCAGTGGATGATGACATGAGCGCGTGGAGG 200
QY 875 gacatctgacacggaagcgtcatgtggaatcagaaacatacagacatactatccgaa 934
Db 199 GCCACATTCACAGTGAATGCTGATGCTGAATCTTGCCTACCCGAGNATTTCCAAACA 140
QY 935 tgactcagaggaatttcgacatcgcactgaatcagcgcgtcaatcagaggggttacgaca 994
Db 139 TGACATCCCGAGGAATTGTGGAGAAACTAACCAAGCCACTGAAAGACACCCCTGAGGAGA 80
QY 995 ttaaccacgctcgtatccggaggagatatacaggaggccactcgcctcagatcagtg 1054
Db 79 -----CAGGAGGCTTCCAGGAGGCACNGCTGGCCTTTTGATGCCATCT 38
QY 1055 ggaagtgtgcttggcttcaacaagaccatggaag 1091
Db 37 GGGCCTTGGNACTGGCCCTGAACAAGACATTTGGAGG 1

RESULT 12
LOCUS B1037782/c 445 bp mRNA EST 14-JUN-2001
DEFINITION CM4-NT0291-150101-663-g08 NT0291 Homo sapiens cDNA, mRNA sequence.
ACCESSION B1037782
VERSION B1037782.1 GI:14444408
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 445)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-NT0291-
150101-663-g08&t3=2001-01-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 445.
Location/Qualifiers
1. .445
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0291"
/dev_stage="Adult"
/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters' patent application
```

```
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 115 a 116 c 114 g 100 t
ORIGIN

Query Match 4.1%; Score 103.4; DB 11; Length 445;
Best Local Similarity 57.6%; Pred. No. 1.8e-18;
Matches 185; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 1878 tgatattaaaatacctccagagcttgagcattgtgaaagtcacacaaactccatgtggtt 1937
Db 402 TGACGCTCTATTCTGCCCCAGCTGGAGCATTCAGCTCCAGGAAGATGAATACATGGCT 343
QY 1938 gggctcttatacggcttcaaggggcctaactcctggtgttggcctctttttggcgtaagga 1997
Db 342 TGGCATTTTCTATGTTTACAAGGGCTGCTGCTGTGTGGGAATCTTCCCTTTCCTATTGA 283
QY 1998 gacgcgtccattaaagtgaacagatcaacgattcgcgttatgtggcgcatcagcatc 2057
Db 282 GACCAAGAGTGTGTCCACTGACAGATCAATGATCACCGGGCTGTGGGATGGCTATCTA 223
QY 2058 taacgtgtcgtcctttgcttgataaacagctccggtgggcatggtcattgcatcgaaca 2117
Db 222 CAATGTGGCAGTCTGCTGCTCATCTGCTCTGTCCATGATTTCTGTCCAGCCAGCA 163
QY 2118 ggaacgctccttgccttgcttgctcagctgctgataattctgtttcctcaagcatgct 2177
Db 162 GGATCAGCCTTTGCTTGTGCTCTCTCTGCCATAGTTTTTCTCCTCTATATCATCTTGT 103
QY 2178 gctgatatattgtccaaagg 2198
Db 102 TGTGCTCTTTTGGCCCCAAGAT 82

RESULT 13
LOCUS BG820975 665 bp mRNA EST 22-MAY-2001
DEFINITION 602780703P1 NCI-CGAP-Brn67 Homo sapiens cDNA clone IMAGE:4931688
5', mRNA sequence.
ACCESSION BG820975
VERSION BG820975.1 GI:14168562
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 665)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10856 row: e column: 01
High quality sequence start: 2
High quality sequence stop: 560.
Location/Qualifiers
1. 665
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4931688"
/clone_lib="NCI CGAP Brn67"
/tissue_type="anaplastic oligodendroglioma with lp/19q
loss"
```

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/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP library."
155 a 186 c 177 q 147 t
BASE COUNT

```

```

BASE COUNT      155 a      186 c      177 g      147 t
ORIGIN
Query Match      4.0%; Score 100.6; DB 11; Length 665;
Best Local Similarity 51.0%; Pred. No. 1.2e-17;
Matches 289; Conservative 0; Mismatches 274; Indels 4; Gaps 2;

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Qy	1803	ctcattgacagatcttttgatccgctgcagcggttatctcgaaacattccccactcsaagatcc	1862
Db	2	CACGGGTCCGATCTGTGGAGCCCTCTGACCGGACCAATTGAGACATTTTGCCAAGGAAACC	61
Qy	1863	agtatctactactgatgattaaaaacgtccagagcttgagcattgtgaaagtccaag	1922
Db	62	TAAGGAGATATTGAGC---TCTCTATTCTGCCCCAGCTGGAGCATTTGCAGCTCCAGGAA	118
Qy	1923	caactcccatgtggttggtcttggtatacggcttcaaggggctaaactctggtgtttggcct	1982
Db	119	GATGAATACATGCGCTGGCATTTTCTATGGTTACAAAGGGCTGCTGCTGCTGCTGGGAAT	178
Qy	1983	cttttggcgctacgagacgcgtccattaaagtgaacagatcaacgattcgcggttat-g	2041
Db	179	CTCTCCTTGCTTATGAGACAAGAGTGTGCCACTGAGAAGATCAATGATCACCGGGCTAG	238
Qy	2042	tggcgatgagcatctataacgtggtgctcttttgcctgataacagctccggtggcgcatgg	2101
Db	239	TGGGCATGGCTATCTACAAATGTGGCAGTCCCTGTGCCCTCATCTGCTCTGTCTCACCATGA	298
Qy	2102	tcatgtcatcgcaacgagacgcgtcttggctctgttgcctagctgtgatatcttgtt	2161
Db	299	TTCTGTCCAGCCAGCAGGATGCAGCCTTTGGCTTTGCCCTCTCTTGGCCATGATTTTCTCCT	358
Qy	2162	gtttcctaagcatgctgtgatattgtgtgccaaagtcattgaggttatcgtcatccca	2221
Db	359	CCTATATCACCTCTTGTAGTGTCTTTGTGCCCAAGATGCGAGGCTGATCACCCGAGGGG	418
Qy	2222	aggataagggcgaatcgaatacaaatccgatttcagccatatcgaagaaggagcgaagaac	2281
Db	419	AATGCGATGTCGGAGCGCAGGACACCATGAAGACAGGGTTCATCGACCAACAACAGCAGG	478
Qy	2282	gctatcagaaaacttgtttaccgaaaaacgagcaattgcaacgatttaataacacagaagaagg	2341
Db	479	AGGAGAAAGTCCCGGCTGTTGGAGAGGAGAACCGTGAACCTGGACCAGATCATTTGCTGAGA	538
Qy	2342	aaaagattcagttcctgcgacagcgtc	2368
Db	539	CAGAGAGGCGTCTCTCTGAACCTGCGCC	565

RESULT	14
AL602784	
LOCUS	335 bp mRNA EST 14-AUG-2001
DEFINITION	DRFZP686J2116_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
ACCESSION	AL602784
VERSION	AL602784.1
KEYWORDS	GI:15166290
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
COMMENT	1 (bases 1 to 335)
	Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
	EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
	Unpublished (1999)
	Contact: Wambutt R
	MIPS
	An Klopferspitz 18a D-82152 Martinsried, Germany

This is the 5' sequence of the clone insert. Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the CDNA sequencing consortium of the German Genome Project. No sl sequence available.

This clone (DKFzp686J2116) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
SOURCE

2:

RESULT 15
AL042317

AL042317	AL042317	459 bp	EST	29-FEB-2000
LOCUS	DXFZp434N0320_r1	434	mRNA	
DEFINITION	DXFZp434N0320_r1 434 (synonym: htes3) Homo sapiens cDNA clone			
	DXFZp434N0320_5', mRNA sequence.			

AL042317
 AL042317.1 GI:5421659
 EST.
 human

SOURCE ORGANISM

Eumkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 459)
Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.

TITLE EST (Ottewaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Ottewaelder B
MIPS

Am Klopferspitz 18a D-82152 Martinsried, Germany

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2002, 01:49:00 ; Search time 101.45 seconds
(without alignments)
5632.371 Million cell updates/sec

Title: US-09-715-962-1

Perfect score: 2523

Sequence: 1 atgcgaagaatgacaag.....caatcacacaagttagtag 2523

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	162.2	6.4	2887	3	US-09-183-253-1
2	132.8	5.3	1318	3	US-09-183-253-3
3	79.2	3.1	397	4	US-08-905-223-3
4	51.8	2.1	7218	1	US-08-232-463-14
5	39.2	1.6	248	4	US-09-007-005-32
6	39.2	1.6	248	4	US-09-244-796-32
7	39.2	1.6	277	4	US-09-007-005-3
8	39.2	1.6	277	4	US-09-244-796-3
9	35.8	1.4	748	1	US-08-361-467B-3
10	35.8	1.4	748	1	US-08-484-332C-3
11	35	1.4	3344	1	US-07-118-575-13
12	35	1.4	3344	1	US-08-481-206-13
13	35	1.4	3344	2	US-08-486-269A-13
14	34.6	1.4	721	4	US-08-998-416-803
15	34.6	1.4	2533	3	US-08-646-273-24
16	34.6	1.4	2720	3	US-08-646-273-35
17	34	1.3	2249	3	US-08-860-635A-18
18	33	1.3	4865	3	US-08-894-017-24
19	33	1.3	5177	6	5352450-1
20	32.8	1.3	12145	3	US-08-968-563-19
21	32.8	1.3	12145	3	US-08-969-683A-19
22	32.6	1.3	289	4	US-09-007-005-17
23	32.6	1.3	289	4	US-09-244-796-17
24	32.6	1.3	1703	3	US-08-646-273-18
25	32.6	1.3	2129	3	US-08-646-273-22
26	32.6	1.3	2314	3	US-08-646-273-29
27	32.6	1.3	2889	1	US-08-289-112-1

Query Match 6.4%; Score 162.2; DB 3; Length 2887;
Best Local Similarity 49.2%; Pred. No. 7.4e-42;

28 32 1.3 30001 1 US-08-125-468-1 Sequence 1, Appli
29 32 1.3 30001 2 US-08-474-933-1 Sequence 1, Appli
30 31.8 1.3 802 4 US-08-896-164-12 Sequence 12, Appli
31 31.8 1.3 4403765 4 US-09-103-840A-2 Sequence 2, Appli
32 32 1.3 460 2 US-08-487-727A-1 Sequence 1, Appli
33 31.6 1.3 1753 4 US-08-205-697A-6 Sequence 6, Appli
34 31.6 1.3 1753 4 US-08-702-525-6 Sequence 6, Appli
35 31.6 1.3 1753 5 PCT-US95-02576-6 Sequence 6, Appli
36 31.6 1.3 2149 1 US-08-784-651-3 Sequence 3, Appli
37 31.4 1.2 2333 1 US-08-427-993B-2 Sequence 2, Appli
38 31.4 1.2 2333 2 US-08-478-609A-2 Sequence 2, Appli
39 31.2 1.2 1605 4 US-09-124-541-3 Sequence 3, Appli
40 31.2 1.2 2730 3 US-08-936-135-17 Sequence 17, Appli
41 31.2 1.2 2781 3 US-08-936-135-19 Sequence 19, Appli
42 31.2 1.2 3607 1 US-08-847-351B-1 Sequence 1, Appli
43 31.2 1.2 9997 1 US-08-246-982A-15 Sequence 15, Appli
44 31.2 1.2 9997 1 US-08-453-265-15 Sequence 15, Appli
45 31.2 1.2 10103 2 US-08-457-273B-7 Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-183-253-1
; Sequence 1, Application US/09183253
; Patent No. 6043054
; GENERAL INFORMATION:
; APPLICANT: VAWTER, LISA
; APPLICANT: STAMMERS, MELANIE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09183,253
; FILING DATE: 30-OCT-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9817907.0
; FILING DATE: 17-AUG-1998
; APPLICATION NUMBER: 60/075,306
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70395
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2887 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-183-253-1

QY	1212	caagttccaggcgatcgctattgctcttacacagatcgaaacagatgatgaacgccaagta	1271
Db			
Db	423	CCGGAAAT--GGGGAGAGAAATGGGGACCAATTAATTTTACTCAATTTTCAAGACAGCAGGGA	479
QY	1272	cgaagattgggttactacgatactcagtttgatgaacattcctggttgaat--actga	1328
Db			
Db	480	GGTGAAGGTGGGAGAGTACAAGCTGTGGCGGACACACTGGAGATCATCAATGACACCAT	539
QY	1329	acagtggtattggtggcaaggttctcaagatcgcaaatgttcacccatgttctaagcac	1388
Db			
Db	540	CAGGTTTCCAAGGATCGGAACCAACCAAAAGACAAGACCATCTCTGGAGCAGCTCGGAA	599
QY	1389	cgtgtccttgccaattatttgtgtgcatgtgcacaatatccagttgtggcataatcgttgc	1448
Db			
Db	600	GATCTCCCTACCTCTCTACAGCATCCTCTCTGCCCTTCACCATCTCTCGGATGATCATGGC	659
QY	1449	cttcgcttgatcatctttaaataatggaataagcatagaagtaagtaatacaatcctcgca	1508
Db			
Db	660	CAGTGGCTTTTCTCTCTTCCACATCAAGAACCGGAATCAGAGCTCATAAAGATGTCGAG	719
QY	1509	tccggtttgcaatacagatcatgttatttggctcatctctgtcctaattctgtcatctt	1568
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Db	720	TCCATACATGAACAACCTTTATCATCCTTGGAGGATGCTCTCCTATGCTTCCATATTCT	779
QY	1569	actgggcatcgacggacgcttctgaagcccgaggaaatatccaaagatatgtcaagcgcg	1628
Db			
Db	780	CNTTGGCCTTGATGGATCCTTTGTCTCTGAAAGAACCTTTTGAACACATTTTGCACCGTCAG	839
QY	1629	ggcttgggttactatccacggttttacctagcatcacgtgtctatgtttcagaaggtctg	1688
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Db	840	GACCTGGATCTTCACCGTGGGCTACAGCAGCGTTTGGGGCCATGTTTGCAAAAGACCTT	899
QY	1689	gggtgtgcatcgtttttacacaaaagcaaaactgacccaaagaaaaagtgaaaccttg	1748
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Db	900	GAGAGTCCACGCCATCTTCAAAAATGTGAAATGAAGAAGAGATCATCAAGGACC--A	956
QY	1749	gaagctatacacatggtttcgggctattatacatagatttagtgatattactctcatg	1808
Db			
Db	957	GAAACTGCTTGTATCGTGGGGGGCATGCTGTGATCGACCTGTGTATCCTGATCTGCTG	1016
QY	1809	cgagatctttgtacgctgcagcgttatctcgaaacattcccaactcgagatccagtatc	1868
Db			
Db	1017	GCAGCTGTGGACCCCTCGGAAGACACTGGAGAGTACAGCATG--GAGCCGACCC	1073
QY	1869	tactactgatataataaatcgtctcagagcttgagcatgtgaaagtcaacgcaactc	1928
Db			
Db	1074	AGCAGGACGGGATATCTCCATCCGCCCTCTCTCTGGAGCACTGTGAGAACACCCATATGAC	1133
QY	1929	catgtggttgggtctgtatacggcttcaaggggctaatcctcgtgttttggcctctttt	1988
Db			
Db	1134	CATCTGGCTTGGCATCGTCTATGCGCTACAAGGACCTTCTCATGTTGTTCGGTGTTCCT	1193
QY	1989	ggcgtacgagacgctctccattaaagtgaacagatccaacgattcgcgttatgtgggcat	2048
Db			
Db	1194	ASCTTGGGAGACCGCAAGCTCAGCATCCCCGCATCCCGCATCAACGACGCAAGTACATCGGAT	1253
QY	2049	gagcatctataacgttggtcgctcttt	2074
Db			
Db	1254	GAGTGTCTACAACGTTGGGATCATCT	1279

ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-3505

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905.223
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 216:
SEQUENCE CHARACTERISTICS:
LENGTH: 397 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
TISSUE TYPE: Brain
FEATURE:
NAME/KEY: other
LOCATION: complement(223..398)
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 96
OTHER INFORMATION: region 111..286
OTHER INFORMATION: id HSGT545
OTHER INFORMATION: est
FEATURE:
NAME/KEY: other
LOCATION: complement(69..219)
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 92
OTHER INFORMATION: region 291..441
OTHER INFORMATION: id HSGT545
OTHER INFORMATION: est
FEATURE:
NAME/KEY: other
LOCATION: complement(2..43)
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 97
OTHER INFORMATION: region 467..508
OTHER INFORMATION: id HSGT545
OTHER INFORMATION: est
FEATURE:
NAME/KEY: other
LOCATION: complement(223..311)
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 92
OTHER INFORMATION: region 4..92
OTHER INFORMATION: id AA036134
OTHER INFORMATION: est
FEATURE:
NAME/KEY: other
LOCATION: complement(46..163)
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 91
OTHER INFORMATION: region 133..250
OTHER INFORMATION: id AA036839
OTHER INFORMATION: est
FEATURE:

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NAME/KEY: other
LOCATION: complement(223..295)
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 97
OTHER INFORMATION: region 1..73
OTHER INFORMATION: id AA038839
OTHER INFORMATION: est
FEATURE:
NAME/KEY: other
LOCATION: 326..387
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 91
OTHER INFORMATION: region 2..63
OTHER INFORMATION: id W51392
OTHER INFORMATION: est
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 152..268
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 5.9
OTHER INFORMATION: seq SVSLSLGIVLA/VV
US-08-905-223-216
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Query Match 3.1%; Score 79.2; DB 4; Length 397;

Best Local Similarity 50.9%; Pred. No. 1.4e-15; Matches 201; Conservative 3; Mismatches 190; Indels 1; Gaps 1;

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QY 1181 aattctgggtggtcgggtggtggtcattcagttctcaggcgcatgctattgctctta 1240
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Db 1 ACITTAGGGTGTCTCTGGCCATGTGCTTTGTATGCCAGCBGCTCTCGATGGCATGGA 60

QY 1241 cacagatgaacagatgatagacgcaagatgaggaagttgggttactacgatactcagt 1300
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Db 61 CGCTTATCAGCAGCTTCAGGCTGCGCAGCTACAAGAGATTGGCTACTATGACAGCACCA 120

QY 1301 tggataacctatctggttgtaactgaacagtggtggtggtggtggtggtggtggtggt 1360
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Db 121 AGGATGATCTTCTGTCGTCACAGATAAATGATTTGGAGGGTCCCGCCAGCTGRSC 180

QY 1361 gcaaatgtcaccatgttctagcaccgtgctctgcttccattattgtgcatgtgca 1420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 AGACCTGGTGTATCAAGACATTCGCTTCCTGCTACAG-ANNNCITTTATCTCCGCTCAG 239

QY 1421 caatatcagttggtgcatctgctgcttgcctgctgctgctgctgctgctgctgctgct 1480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 240 TTCTCTCAGCCTGGCATTTGCTAGCTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 299

QY 1481 agcatagaagagtaatacaactcctgcatcccggttgcgaatacagatcatgttattggtg 1540
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 300 CACATGTCCGTTATATCCAGAACTCACAGCCCAACCTGAACACCTGACTGTGTGGGCT 359

QY 1541 tcatactgtcctaatactatctatcttactgggc 1575
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Db 360 GCTCMTGGCTTACTGCTGTCTTCCCTCTGGGC 394
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RESULT 4
US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
```

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ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-Fls
US-08-232-463-14
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Query Match 2.1%; Score 51.8; DB 1; Length 7218;

Best Local Similarity 6.3%; Pred. No. 7.6e-06; Matches 26; Conservative 215; Mismatches 172; Indels 0; Gaps 0;

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QY 791 ggtcagaggaactggtacgagtgatctgaaagcagagggcgcacacgtgctgtg 850
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Db 1430 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1371

QY 851 aacagatgcgaatagtcgcgaagggacatctgacaacggaagcgctcatgtcggaatcaga 910
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1370 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1311

QY 911 acaatcagacaactatccggaatgactgcagaggaaatttcgacatcgactgaatcagg 970
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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QY 971 cgctaactcagaggggttacgacattaccacgacgcgtatccggagggaatcagagg 1030
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Db 1250 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1191

QY 1031 cgccactgcctacgacgtcagtggtgagtggtggttggcttcaacaagaccatggaac 1090
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Db 1190 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1131

QY 1091 gaitgacaacccgggaagaaatctctgagggatttaccatatacgcgaagagattgccg 1150
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Db 1130 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1071

QY 1151 atgaatctacgctgcctgaactccacacaaattctcgggtggtggtggtggtg 1203
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1070 RRRATCCGACGCTCCCTCGACCTGCAGCCAGCTCGGAATTAATTCGTGAG 1018
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RESULT 5
US-09-007-005-32
Sequence 32, Application US/09007005B
Patent No. 6258558
GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
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RESULT

0.

RESULT 6

RESULT

 \ddot{O}

RESULT 12
US-08-481-206-13
; Sequence 13, Application US/08481206
; Patent No. 5739291
; GENERAL INFORMATION:
; APPLICANT: Heinemann Ph.D., Stephen F.
; APPLICANT: Boulter Ph.D., James R.
; APPLICANT: Hollmann Ph.D., Michael NMN
; APPLICANT: Bettler Ph.D., Bernhard NMN
; APPLICANT: Jensen Ph.D., Jan E.
; TITLE OF INVENTION: GLUTAMATE RECEPTOR COMPOSITIONS AND
; METHODS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 So. Flower St., Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,206
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/013,767
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter Ph.D., Stephen E.
; REGISTRATION NUMBER: 31192
; REFERENCE/DOCKET NUMBER: P31 8962
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; TELEX: 9103330318
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3344 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; CELL TYPE:
; CELL LINE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Glur7
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2766
US-08-481-206-13

Query Match 1.4%; Score 35; DB 1; Length 3344;
Best Local Similarity 45.9%; Pred. No. 1.2;
Matches 119; Conservative 0; Mismatches 140; Indels 0; Gaps 0;
QY 36 gttttgatatattttgtttgttttaatcgctcgccgcaacgtgcaagggcggtgagcggg 95
Db 39 GGTGTTGGGAATACTGGGCGGGTTCCTGCTGCGCCTTCGGATCCAGACTCGCGCGG 98
QY 96 gaggcccgatgaactgcacatcgccgcatctttccgatagccgcaagaggatggca 155
Db 99 GATGCCCCAGCATCGCGGATCGCGGAATCTTTGATACGCGGAGCGGCCCAAGGCCCA 158
QY 156 gggcgccagcggtgatgctgctgcccacaagactggtggtgatggtcacaacagagcc 215

Db 159 GGTCAATGAACGCTGAGGAGCACCCTTTTCGGTTTTCTGCCAATATCATCAACAGGACAG 218
QY 216 gaatctgtgcggggcttcaagctcatctgcacagcagcagcagcagcagcagcagcgg 275
Db 219 AACTCTGTGTCCTCAACACAGCAGCCTGACCTAGCAGATTTCAGAGGATTTCACCTTCCATGACAG 278
QY 276 ttggggcgccagcggatg 294
Db 279 TTTTGAGGCCACCACAAG 297
RESULT 13
US-08-486-269A-13
; Sequence 13, Application US/08486269A
; Patent No. 5945509
; GENERAL INFORMATION:
; APPLICANT: Heinemann, Stephen F.
; APPLICANT: Boulter, James R.
; APPLICANT: Hollmann, Michael
; APPLICANT: Bettler, Bernhard
; APPLICANT: Jensen, Jan E.
; TITLE OF INVENTION: GLUTAMATE RECEPTOR COMPOSITIONS
; AND METHODS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows DEMONSTRATION Version 2.0D
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,269A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/013,767
; FILING DATE: 04-FEB-1993
; APPLICATION NUMBER: 07/718,575
; FILING DATE: 21-JUN-1991
; APPLICATION NUMBER: PCT/US90/06153
; FILING DATE: 25-OCT-1990
; APPLICATION NUMBER: 07/428,116
; FILING DATE: 27-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9986
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3344 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: Glur7
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...2763
; OTHER INFORMATION:
US-08-486-269A-13

RESULT 15

US-08-646-273-24/c
; Sequence 24, Application US/08646273
; Patent No. 6066502

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/03706
; FILING DATE: 11-NOV-1994
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2533 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA for mRNA
; US-08-646-273-24

Query Match          1.4%; Score 34.6; DB 3; Length 2533;
Best Local Similarity 51.6%; Pred. NO. 1.4;
Matches 79; Conservative 0; Mismatches 74; Indels 0; Gaps

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QY 695 tgggactctctatgtggtggccgcagagaggtgctctgcgaaatgtacaaacagcgc 754
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Db 1460 TTGGGGGCTTTTCTTGAGCTGATGCGGAGTGACCCCTCCATGAGAGATTGAAAACCGCATG 1401
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Db 1400 GCATTTTCAAGTAGAGGCTGGAACCTCCAGTG 1368
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Search completed: May 1, 2002, 04:25:03
Job time: 9363 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2002, 02:48:15 ; Search time 231.77 Seconds
(without alignments)
9332.664 Million cell updates/sec

Title: US-09-715-962-1
Perfect score: 2523
Sequence: 1 atgcgaagatgacaag.....caatcacacaagtgagtag 2523

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS1/gcgdata/geneseq/geneseq/NA1981.DAT.*
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13: /SIDS1/gcgdata/geneseq/geneseq/NA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseq/NA1993.DAT.*
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17: /SIDS1/gcgdata/geneseq/geneseq/NA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseq/NA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq/NA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq/NA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	571.4	22.6	2895	20	AAH20519
3	570.6	22.6	2886	22	AAH20519
4	569.4	22.6	2535	20	AAH20519
5	569.4	22.6	2602	20	AAH20519
6	569.4	22.6	2620	19	AAH20519
7	569.4	22.6	2679	20	AAH20519
8	569.4	22.6	2700	20	AAH20519
9	569.4	22.6	2822	21	AAH20519
10	569.4	22.6	2886	20	AAH20519
11	569.4	22.6	2886	20	AAH20519

12	569.4	22.6	2887	20	AAH20519	Human GABABR1b rec
13	569.4	22.6	2914	21	AAH20519	Human GABABR1a rec
14	569.4	22.6	2924	19	AAH20519	Human GABA-BR1b re
15	569.4	22.6	3464	20	AAH20519	Human GABABR1a rec
16	569.4	22.6	3464	20	AAH20519	Human GABABR1a cod
17	569.4	22.6	3569	20	AAH20519	GABA-BR1a*Gqo5 fus
18	569.4	22.6	4565	22	AAH20519	Human brain cell s
19	566.8	22.5	4220	20	AAH20519	Human GABA B recep
20	563.6	22.3	4220	22	AAH20519	Human GABA-B-R1a c
21	558	22.1	2883	20	AAH20519	Murine gamma-amino
22	558	22.1	2883	22	AAH20519	Murine GABA-B-R1a
23	554.8	22.0	2532	20	AAH20519	Rat GABABR1b codin
24	554.8	22.0	2837	19	AAH20519	Rat GABA-BR1b rece
25	554.8	22.0	2880	20	AAH20519	Rat GABABR1a codin
26	554.8	22.0	4376	19	AAH20519	Rat GABA-BR1a rece
27	553	21.9	2661	20	AAH20519	Human GABAB recep
28	523.8	20.8	2518	20	AAH20519	Human GABAB recep
29	520.8	20.6	3127	20	AAH20519	Human GABABR1b cod
30	392	15.5	1746	20	AAH20519	Canine GABAB recep
31	374.4	14.8	1386	20	AAH20519	Human GABAB recep
32	374.4	14.8	1737	20	AAH20519	Human GABAB recep
33	338.2	13.4	2367	20	AAH20519	Human GABAB recep
34	337.8	13.4	2489	20	AAH20519	Human GABAB recep
35	271.4	10.8	1692	20	AAH20519	Human GABAB recep
36	222.4	8.8	5459	21	AAH20519	Rat gb2 GABA B rec
37	220.2	8.7	2823	21	AAH20519	Rat gamma amino bu
38	219.2	8.7	3288	21	AAH20519	Rat GABA-B recepto
39	219.2	8.7	3288	21	AAH20519	Rat GABA-B recepto
40	218.6	8.7	2652	20	AAH20519	Rat GABABR2 coding
41	211.6	8.4	3256	21	AAH20519	CDNA encoding a hu
42	210	8.3	2823	20	AAH20519	Human partial GABA
43	210	8.3	2826	21	AAH20519	Human GABA-B recep
44	210	8.3	2826	21	AAH20519	Human GABA-B recep
45	210	8.3	2826	21	AAH20519	Human GABA-B-R2 re

ALIGNMENTS

RESULT 1
AAH20519
ID AAH20519 standard; DNA; 2523 BP.
AC AAH20519;
DT 03-AUG-2001 (first entry)
DE D. melanogaster GABA-B receptor DNA SEQ ID 1.
XX GABA-B receptor; fruitfly; gamma-aminobutyric acid B receptor;
KW insecticide; transgenic invertebrate; plant protection agent;
KW human medicine; veterinary medicine; insect; ds.
XX Drosophila melanogaster.
XX DE19955408-A1.
PD 23-MAY-2001.
XX 18-NOV-1999; 99DE-1055408.
PR 18-NOV-1999; 99DE-1055408.
PA (FARB) BAYER AG.
XX Raming K, Mezler M, Mueller T;
XX WPI: 2001-318282/34.
XX P-PSDB; AAB86159.

New invertebrate gamma-aminobutyric acid receptor proteins, useful in screening for potential insecticides, for plant protection or medicine, also related nucleic acid

XX Claim 6; Page 8-15; 62pp; German.
PS This invention describes a novel polypeptide (I), functioning as a
XX gamma-aminobutyric acid -B (GABA-B) receptor which has insecticidal
CC activity. (I), also the nucleic acid (II) that encodes it and related
CC vectors, host cells, antibodies and transgenic invertebrates, are used
CC for identifying: (i) new plant protection agents, i.e. modulators of (I)
CC with insecticidal activity, which may also be useful in human or
CC veterinary medicine; and (ii) genes that encode polypeptides involved in
CC assembly of functionally related GABA-B receptors in insects. This
CC sequence encodes a fruitfly (Drosophila melanogaster) GABA-B receptor
XX which is described in the method of the invention.
SQ Sequence 2523 BP; 650 A; 605 C; 653 G; 615 T; 0 other;

Query Match 100.0%; Score 2523; DB 22; Length 2523;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atgcgcaagatagacaagtgtgctgttactgcttttggatatttttggcttttta 60
Db 1 atgcgcaagatagacaagtgtgctgttactgcttttggatatttttggcttttta 60

Qy 61 atgccttcgcgcacctgcaaggggcgctgcccggaggcccgatgaactgcacatcgcc 120
Db 61 atgccttcgcgcacctgcaaggggcgctgcccggaggcccgatgaactgcacatcgcc 120

Qy 121 ggcattcttcgcatagccgcgcaaaaggagatggcaggccgagcgctgtatgctgcc 180
Db 121 ggcattcttcgcatagccgcgcaaaaggagatggcaggccgagcgctgtatgctgcc 180

Qy 181 acaagactggcgttgatgtatgcacaaagcagcgcgaatctctcggcgctccaagctc 240
Db 181 acaagactggcgttgatgtatgcacaaagcagcgcgaatctctcggcgctccaagctc 240

Qy 241 atcctgcacagcaacgacagcgagtgtgagccgggttggcgccagcggtgatgacaat 300
Db 241 atcctgcacagcaacgacagcgagtgtgagccgggttggcgccagcggtgatgacaat 300

Qy 301 ctgctctataataaccgcgaagctgatgtgttggcaggatgacagcagctctgcacc 360
Db 301 ctgctctataataaccgcgaagctgatgtgttggcaggatgacagcagctctgcacc 360

Qy 361 actgtagccggcgtgcgcaaaatgtggaatctaatgtgctctctacgggaccccgagt 420
Db 361 actgtagccggcgtgcgcaaaatgtggaatctaatgtgctctctacgggaccccgagt 420

Qy 421 ccggctcttcggatcgcaaacgattcccaactctatccgcaccatccatcgccacg 480
Db 421 ccggctcttcggatcgcaaacgattcccaactctatccgcaccatccatcgccacg 480

Qy 481 gtgcacaaatcaacgcgcataacgctgatgaagaataatcgctgttccgggtggccatt 540
Db 481 gtgcacaaatcaacgcgcataacgctgatgaagaataatcgctgttccgggtggccatt 540

Qy 541 ctgcagcagcgaggaggtctttatctcgaccgttagaggatctcgagaatcgatgcag 600
Db 541 ctgcagcagcgaggaggtctttatctcgaccgttagaggatctcgagaatcgatgcag 600

Qy 601 gaggctggcgttgaatcgttaactagacaatcttctatccgatcccaacagacgcgctg 660
Db 601 gaggctggcgttgaatcgttaactagacaatcttctatccgatcccaacagacgcgctg 660

Qy 661 cgcattttgcagcgcaggatgcagcatcatttgcggacttctatgtggtggccgcc 720
Db 661 cgcattttgcagcgcaggatgcagcatcatttgcggacttctatgtggtggccgcc 720

Qy 721 aggagggctcctgcgaaatgtacaaacagcagctatgcccggagctcatgtgtggttc 780
Db 721 aggagggctcctgcgaaatgtacaaacagcagctatgcccggagctcatgtgtggttc 780

Qy 781 tttattggctgttacgaggaacaactggttacgaggtgaatctgaagcagagggcatcacc 840
Db 781 tttattggctgttacgaggaacaactggttacgaggtgaatctgaagcagagggcatcacc 840

Qy 841 tgcactgttgaacagatggaatagctgccgaaggacatctgacaacggaagcgtcatg 900
Db 841 tgcactgttgaacagatggaatagctgccgaaggacatctgacaacggaagcgtcatg 900

Qy 901 tggatcagaacaatcagacaactatccggaatgactgcagagggaatttcacatcga 960
Db 901 tggatcagaacaatcagacaactatccggaatgactgcagagggaatttcacatcga 960

Qy 961 ctgaatcaggcgttaatcagagggggttacgacattaacaccatcgctatccggagga 1020
Db 961 ctgaatcaggcgttaatcagagggggttacgacattaacaccatcgctatccggagga 1020

Qy 1021 tatcaggaggcgcactcgctacgacgatgcagtgagggtggttggcttttcaacaag 1080
Db 1021 tatcaggaggcgcactcgctacgacgatgcagtgagggtggttggcttttcaacaag 1080

Qy 1081 accatggaacgattgacaacccgggagaatactctgagggttttacctatacaggacaag 1140
Db 1081 accatggaacgattgacaacccgggagaatactctgagggttttacctatacaggacaag 1140

Qy 1141 gagattgcccgtgaaatctacgtgcgaactcacaacaaattctgggtgtatcggt 1200
Db 1141 gagattgcccgtgaaatctacgtgcgaactcacaacaaattctgggtgtatcggt 1200

Qy 1201 gfggtggcattcagctcaggcgcatctattgctcttacagatcgacaacagatgata 1260
Db 1201 gfggtggcattcagctcaggcgcatctattgctcttacagatcgacaacagatgata 1260

Qy 1261 gacggcaagtcagcagaagttgggttactacgatactcagttggataacacctatcctgtg 1320
Db 1261 gacggcaagtcagcagaagttgggttactacgatactcagttggataacacctatcctgtg 1320

Qy 1321 aatactgaacagtggaattggtggcaaggttccctcaagatcgacaattgtcaccatgtt 1380
Db 1321 aatactgaacagtggaattggtggcaaggttccctcaagatcgacaattgtcaccatgtt 1380

Qy 1381 ctacgcacgctgcttggcattatttggatgtgcagtgacaataatccagttgtggcata 1440
Db 1381 ctacgcacgctgcttggcattatttggatgtgcagtgacaataatccagttgtggcata 1440

Qy 1441 ttcgttgccttcgcttgatcatcttaataatggaataagcatagaagaagtaatacaa 1500
Db 1441 ttcgttgccttcgcttgatcatcttaataatggaataagcatagaagaagtaatacaa 1500

Qy 1501 tccctgcacccgcttggcaatacagcatcttatttgggtgctcatctgtcttaatatct 1560
Db 1501 tccctgcacccgcttggcaatacagcatcttatttgggtgctcatctgtcttaatatct 1560

Qy 1561 gtcatttactgggcatcgacgacgcttggcagccccggaggaataatcccaagatatgt 1620
Db 1561 gtcatttactgggcatcgacgacgcttggcagccccggaggaataatcccaagatatgt 1620

Qy 1621 caagcgcggcttgggttactatccacgggttttacactagcatcagctgtctatgttcagc 1680
Db 1621 caagcgcggcttgggttactatccacgggttttacactagcatcagctgtctatgttcagc 1680

Qy 1681 aaggctggcgtgtgcatcgttttacaacaaagcaaaaactgacccaaagaaaaagt 1740
Db 1681 aaggctggcgtgtgcatcgttttacaacaaagcaaaaactgacccaaagaaaaagt 1740

Qy 1741 gaaccttgaagcgtatcacaccatgggttccggggtattatcaatagatttagtgatatta 1800
Db 1741 gaaccttgaagcgtatcacaccatgggttccggggtattatcaatagatttagtgatatta 1800

Qy 1801 ctctcatggcagatcttggatccgctgcagcgttatctcgaaacattcccacacgaagat 1860
Db 1801 ctctcatggcagatcttggatccgctgcagcgttatctcgaaacattcccacacgaagat 1860

Qy 1861 ccagttactactactgatgatatataaaatcgtccagagcttgagcatgtgaaagctcaa 1920

Db 1072 aagcgccaggatgccgaatacatcgtgggacttttctatgagactgaagcccgaaagtg 1131
Qy 730 ctctgcgaatgtacaacacgacgtatataatggcagagctatgtgtgttctttattggc 789
Db 1132 ttctgtgaggtatacaaggagcgctctctttgggaagatgtgtgtgttctctcattggg 1191
Qy 790 tggtagagacaaactggtacagaggtgaatctgaaagcagagggcatcacctgcactatt 849
Db 1192 tggtagctgacaattgggt-----tcaagacctacgacctccatcaactgcacagt 1245
Qy 850 gaacagatgcgaatagctgcgcgaaggacatctgacaacggaagcgctcatgttggaaatcag 909
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Qy 910 aacaatcagaacaactatctccggaatgactgcagaggaatttcgacatcgactgaaatcag 969
Db 1306 gccaaacccgcagcatctccaacatgacatcccaggagttgtggaagaaactgaccaag 1365
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Db 1366 agact-----caagagacacctgaggagacagcggtctccaggag 1407
Qy 1030 gcgccactgcctacgtacaggtgtgaggtgtgcttttggcttttcaacaagaccatgaa 1089
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Qy 1090 cgattgacaacgggaagaaatctctgagggaatttaccctatacgcgaacagagattgcc 1149
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Qy 1150 gatgaactctacgctgcacataacacaaatctctgggtgtatccgggtgtgtgga 1209
Db 1528 gaccaaatctaccgcgaatgaactcctctgcttggagggtgtctgtgccacgtgggt 1587
Qy 1210 ttcaagtctcaggcgatcgtatgtctctacagatcgacaagatgatagacggcaag 1269
Db 1588 ttgatcccgccgtcacggatggcctggactgtattggagcagctcaggggtggcagc 1647
Qy 1270 tacgagaagtgggttactacgatactcagttggataacacctactcctgttgaatactgaa 1329
Db 1648 tacaagaagatcggtactactatgacagaccaggaatgaccttctctgttctaaaaaggac 1707
Qy 1330 cagtggattgggtgcaaggttctcaagatcgcaaatgtcaacccatgttctacgcacc 1389
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Qy 1390 gtgtccttgccattattgtgtcatgtgcacaatatccagttgtggcatattcttggc 1449
Db 1768 atgtcacagaagctctctcaattcagctctctgtctctccagcctgggcatgtctgtgct 1827
Qy 1450 ttgccttgatcatctttaataataatggaataagcatagaagtaatacaatcctcgcat 1509
Db 1828 gtggtctgtctgtctttaacatctacaactcatatccgtttacatccagaactcccaag 1887
Qy 1510 cccgtttgcaatacagatgtaattgttgggtgtcatcatctgtcttaataatctgtctatcta 1569
Db 1888 cccaacttgaacaactgactgtgtgggtgctccctgcatgtgctgctgctgtcccttcccc 1947
Qy 1570 ctgggcatcacgacgctttgtcagcccccgagggaataatccaaagatatgtcaagcggg 1629
Db 1948 ctggggctagatgggtaccacatcggggaagccaggttctcttgtgtgtcagcagc 2007
Qy 1630 gcttggttactatccacgggttttacactagcatcacggtgtctatgttccagcaaggtctgg 1689
Db 2008 ctctggtcctctgggtctggtctcagttcagttgggtatggtctccatgttccaggaatctgg 2067
Qy 1690 cgtgtgcatcgttt-----tacaacaaaacaaactgaccccaagaaaaagtggaa 1743
Db 2068 tgggtccacacgctcttcaactaagaaggaggaagaagaggtgggaagaccctggag 2127
Qy 1744 ccttgggaagctatacaccaatggttccgggtctattatacaatagatttagtgaatactc 1803
Db 2128 ccctgggaagctgtacacacagtggtgtgtgttagtgggcatgtgtgtctcctactctgcc 2187

Qy 1804 tcatggcagatctttgatccgctgcagcgttatctctcgaaacatttcccactcgaagatcca 1863
Db 2188 atttggcagatgtagacccttgcaccctgacccagaccattgagacttttgcgaaggaggaacca 2247
Qy 1864 gtatctactactgatatataaaatcacgtccagagctgagcatgtgaaagtcaacgc 1923
Db 2248 aaggagaatattgatg---tgtccatctctgccccagctggagcactgcagctccaagaaa 2304
Qy 1924 aactcatgtgtgtgggtctctgtatcacggtctcaagggtggttaactcctggttttggcctc 1983
Db 2305 atgaacacctgctgtggcattttctatgtttacaagggtcgtgctgctgctagggcatc 2364
Qy 1984 ttttggctacgagacgcgctccatataaagtgaacagatcaacagattcgcttattgtg 2043
Db 2365 tttctgtctatgagaccaagagcgtgtctactgagaagatcaatgaccacgggctgtg 2424
Qy 2044 ggcattgagcatctataacgtgtgcttcccttgccttgcctgataacagctccgggtggcagtgctc 2103
Db 2425 ggcattggccatgtacaacgtggcgttctgtgctcactcactgcccgggtccaccatgatc 2484
Qy 2104 attgcatcgcaacagcagcgtcttgccttgccttgccttgccttagcttagcttatctgtgt 2163
Db 2485 ctgtccagccagcagatgcagcttgccttgccttgcagctcttgcctatgctgttctctcc 2344
Qy 2164 ttcttaagcatgctgctgatatatttggccaaaggctcattgaggttatcagctcatcccaag 2223
Db 2545 tacatcactctgctgtctgtctgttgcgtgcgaagatgcgcaggttgatcacccgggtgag 2604
Qy 2224 gataaggcgaatcgaataataacatccgattccgcatcgcataatcgaaaaggagcagaacgc 2283
Db 2605 tggcagtcggaggcgcagatataccatgaaaacgggtgcgtcgaccacaacaatgagaa 2664
Qy 2284 tatcagaactgtttaccgaaaaacgagcaattgcaacgattacaacgataacacagaaggagaa 2343
Db 2665 gagaagcccgactgttgagaaggagaccgggagctggagagatcattgtctgagaaa 2724
Qy 2344 aagattcaggt 2354
Db 2725 gaggagcgaggt 2735

RESULT 3

AAC91925

ID AAC91925 standard; cDNA; 2886 bp.

AC AAC91925;

XX XX

DT 19-MAR-2001 (first entry)

XX Human GABA-B-R1a coding sequence #1.

XX Human; gamma-amino-butyric acid receptor; GABA-B; SS.

XX Homo sapiens.

XX PN WO200073788-A1.

XX PD 07-DEC-2000.

XX PF 30-MAY-2000; 2000WO-CA00638.

XX PR 01-JUN-1999; 99US-0137025.

XX PA (MERI) MERCK FROSST CANADA & CO.

XX PI Ng G, O'Neill G;

XX DR WPI: 2001-049959/06.

XX DR P-PSDB; AAB50090.

XX PT Use of gabapentin, 1-(aminomethyl)cyclohexanecarboxylic acid, in assays for
identifying gamma-amino-butyric acid (GABA)-B agonists and antagonists

PT
XX
PS
XX

Disclosure; Fig 6; 85pp; English.

The present invention relates to a method for determining whether a substance binds to gamma-amino-butyric acid (GABA)-B receptors and is a potential agonist or antagonist of the GABA-B receptor. The method comprises exposing cells to 1-(aminomethyl)cyclohexanecarboxylic acid (gabapentin) in the presence or absence of the substance under investigation. The present sequence is a coding sequence for human GABA-B-R1a, which was used in the present invention to construct a functional GABA-B receptor, for use in the method of the present invention.

XX
SQ Sequence 2886 BP; 632 A; 822 C; 797 G; 634 T; 1 other;

Query Match 22.6%; Score 570.6; DB 22; Length 2886;

Best Local Similarity 54.8%; Pred. No. 1.8e-170;

Matches 1231; Conservative 1; Mismatches 980; Indels 33; Gaps 4;

QY 130 ccgtagccgcgaagagagatgagcagggcgccagcgctgtatgcctgccacaagactg 189
 DB 523 ctgttcccatgagcgggctgcgcagggcgccagcgctgccagccgcgggtgagatg 582
 QY 190 gcgttgatgatgtaacaagcagccgaatctgctgcgggcttcaagctcatctgcac 249
 DB 583 gcgctggagagcgtgaatagccgcagggacatcctccggactatgagctcaagctcatc 642
 QY 250 agcaacgacagcagtgtagccggcttggcgccagcgtgagtgatacaatctgctctat 309
 DB 643 caccagcagcagtgtagtccagggcgaagccaccagctatgagctgctctac 702
 QY 310 aataaacccgaagctgagctgtgtgagcagtgagcagcggctgcaccactgtagcc 369
 DB 703 aagcaccctataagatcatcttattgcctggctgcggctctgtccacagctggggct 762
 QY 370 gagggcccaaaatggaatcattatgtctctgcacgggctgcagctggctctt 429
 DB 763 gagggctgagtgatggaacctatgtgtcttccatggtccagctcaccagccctg 822
 QY 430 tcggatgcgaagcattcccaactctattccgaccatccatccatccgacagcggcgacaat 489
 DB 823 tcaaacggcagcgtttcccaactttctccgaacgcaccatccagcaccactccaac 882
 QY 490 ccaacgcgatcaagctgagtagaagaattcgctggctccggggtggccattctcagcag 549
 DB 883 cctaccgcgctgaacctcttgaaaagctggggctgggaagagtgtctaccatccagcag 942
 QY 550 gcggagaggtctttatccgaccgttagagatctcgagaatcgatgcagtgaggctggc 609
 DB 943 accactgaggtcttccatctcgactctgagcagcctggagaaacgagtgaaagagctgga 1002
 QY 610 gttgaatcgttaactagacaaatcttctatccgatcccaacagacgcggtgcgaatttg 669
 DB 1003 attgagattacttccgcagaggtttctctcagatccagctgtgcccgtcaaaaacctg 1062
 QY 670 cgaacgcagatcacgcacatctgtggactcttctatgtgtggcgcagagaggtg 729
 DB 1063 aagcgcagagatgcgcgaatctatcggtgggactttctatgagactgaagccggaaagt 1122
 QY 730 ctctgcgaatgtacaaacagcagctatatggccgagctcatgtgtgtttttattggc 789
 DB 1123 tttgtgaggtgtacaaagagcgtctcttgggaagaagtacgtctgtgttctcatggg 1182
 QY 790 tggtagagagacactggtagcaggtggaattctgaaagcagagggcacaacctgcactgtt 849
 DB 1183 tggtagctgacaattggt-----tcaagatctacgacctcttatcaactgcacagt 1236
 QY 850 gaacagatgcgaatagctgcgcgaagagacatctgacacgcgaagcgctcatctgtggaatcag 909
 DB 1237 gatgagatgactagggcgtggggggccacatcacaaactgagattgtctgctgaatct 1296

QY 910 aacaatcagacaactatattccggaatgactgcagagaaatttcgacatcgactgaatcag 969
 DB 1297 gccaataccgcgcagcatttcccaacatgacatcccggaatttctggaagaactcaaccaag 1356
 QY 970 gcgctaactgcagaggggttacgcacattaaaccagatcgctatccggaggatatacaggag 1029
 DB 1357 cgactgaaagacacacctgaggaga-----caggaggtctccaggag 1398
 QY 1030 gcgcactgcgtacacgatgcagtgtagagtgtaggttggcttctcaacaagaccatggaa 1089
 DB 1399 gcaacgctggtcctatgatgcctatggccttggcactggcctggaacaagacatctgga 1458
 QY 1090 cgattgacaacccgggaagaaatctctgagggattttacctatatacggacaagagattgcc 1149
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 QY 1210 ttacgttctcagggcgatgtattgtctttacacagatcgaaacagatgatacagcgcaag 1269
 DB 1579 ttgtatgccagcggtctcgatggcagcgttattatcgagcagcttcaggtggcagc 1638
 QY 1270 tacgagaagtgggttactacgatactcagttggtgataaacctatctctggttgaatactgaa 1329
 DB 1639 tacaagaagatggctactatgacagcaccagagatgatcttctcgtgtccaaaacagat 1698
 QY 1330 cagtggattggggcaaggttctcgaagatcgacaattgtcaccatgttctacgacc 1389
 DB 1699 aaatggatggagggttccccccagctgcacagacctggctacagacattcccgttc 1758
 QY 1390 gtgtccttccattattgtgtcatgtgcacaatactccagttgtggcatattcgttgcc 1449
 DB 1759 ctgtcacaagaactcttattctcgtctcagttctctcagcctggcattgttctcagct 1818
 QY 1450 ttgccttgcattcatcttataatataatgaataagcatagataacataactcctgcacat 1509
 DB 1819 gtgtgtctgtccttcttaacatctacaactcaactcagctcgttataccagaactcacag 1878
 QY 1510 cccgtttgcaatacagatactattgtgttcacatctgtctataatctgtcattctta 1569
 DB 1879 cccaactgaaacactgactgctgtgggtgctcactggctttagctgtctctcccc 1938
 QY 1570 ctgggcctgcagcagcgtttgtcagccccgaggaataaccagaatgtatgaagcgcgg 1629
 DB 1939 ctggggctgcagtggttaccacatgggaggaaccagttctcttctgtcgcaggccgcg 1998
 QY 1630 gcttggttactatccaccggttttacactagcatacaggtgtctatgttcagcaaggtctgg 1689
 DB 1999 ctctggctcctggcctggcctttagtctgggtacggttccatgttccaccaagattgg 2058
 QY 1690 cgtgtgcatcgtttttacaacaa-----aagcaaaactgacccccaaagaaaaagtggaa 1743
 DB 2059 tgggtccacacggtcttccaaagaagaagaagagagtgaggaggaactcctggaa 2118
 QY 1744 ccttgaagctatacaccatggttctcgggctattatcaatagatttagtattact 1803
 DB 2119 ccttggaaagctatgcccacagtgggcctgtgtgtgggcatggatgccctctctgcgc 2178
 QY 1804 tcatggcagatcttggatccgctgcagcgttattctcgaaacttcccactcgaagatcca 1863
 DB 2179 atctggcagatcgtggacctctgcacccgaccttgagacatttgcacaggaggaaacct 2238
 QY 1864 gtatctactactgataattaaaaacgtccagagacttgagcattgtgaaagctaacgc 1923
 DB 2239 aaggaagatattgagc---tctctattctgccccagctggagcattgcagctccaggaag 2295
 QY 1924 aactccatgtggttgggtctgttacggttcaaggggcttaactcctgtgtgttggcctc 1983
 DB 2296 atgaatacatgcttggcatttctctatgattacaaggggctgtctgtctgtctggaatc 2355
 QY 1984 tttttggcgtacgagacgcgcgtccctccattaaagtgaacagatcaacgatttcgcgttatgtg 2043

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Db 2356 ttcttctttagagaccacgaagtggtgccactgagaagataaatgataccacggctgtg 2415
QY 2044 ggcattgagcattataacgtgtgtgtcttcttgctgataacacagctccgggtggcattggctc 2103
Db 2416 ggcattgagcattataacgtgtgtgtcttcttgctgataacacagctccgggtggcattggctc 2475
QY 2104 attgcatcgcaaaaggacgcgtcttcttgccttgccttgccttgccttgccttgccttgccttgc 2163
Db 2476 ctgtccagccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2535
QY 2164 ttcttaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2223
Db 2536 tatactactctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2595
QY 2224 gataagcccgcaatgaaatacaataccccgattcagccatcagcaagagagagcaagaacgc 2283
Db 2596 tggcagtcggagcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2655
QY 2284 tatcagaaactgtttaccgaaaaacgagcaattgcaacgatttaataacacagagagagaa 2343
Db 2656 gagaagtcctggctgtgtggaagagagacccgtgaactggaactggaaagatcattgtgagaaa 2715
QY 2344 aagattcagtcctgcgacagcgtc 2368
Db 2716 gagagcgtgtctctgaactgcgc 2740

RESULT 4
ID AAX58055
ID AAX58055 standard; cDNA to rRNA; 2535 BP.
XX
AC AAX58055;
XX
DT 21-JUL-1999 (first entry)
XX
DE Human GABAB receptor lb coding sequence.
XX
KW GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;
KW transient lower oesophageal sphincter relaxation; spasticity; emesis;
KW gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;
KW irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;
KW autoimmune disease; neoplastic disease; infectious disease; therapy; ss.
XX
OS Homo sapiens.
XX
PN WO9921890-A1.
XX
PD 06-MAY-1999.
XX
PF 27-OCT-1998; 98WO-SE01947.
XX
PR 17-JUL-1998; 98SE-0002575.
PR 27-OCT-1997; 97SE-0003914.
PR 16-MAR-1998; 98SE-0000864.
XX
PA (ASTR ) ASTRA AB.
XX
PI Ekstrand J;
XX
DR WPI; 1999-302985/25.
DR P-PSDB; AAY14102.
XX
XX Polynucleotides encoding human and canine gamma aminobutyric acid
PT type B receptors, used to screen for compounds that are inhibitors
PT of transient lower oesophageal sphincter relaxations
XX
PS Claim 6; Page 90-94; 222pp; English.
XX
XX This sequence encodes a human gamma aminobutyric acid type B (GABAB)
CC receptor of the invention. Nucleic acid molecules encoding GABAB
CC receptors can be used to screen for compounds that are inhibitors of
CC transient lower oesophageal sphincter relaxations (TLESR). They can also

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CC be used to screen for agonists or antagonists of the GABAB receptors.
CC Inhibitors of TLESR are useful for treating gastro-oesophageal reflux
CC disease. Other uses of GABAB receptors, such as human GABAB Ric or 1d,
CC comprise diagnosis or treatment of conditions related to GABAB
CC dysfunction, e.g. epilepsy, psychiatric disorders, emesis, irritable
CC bowel syndrome, dyspepsia, spasticity, arthritis, allergies, autoimmune
CC diseases, neoplastic diseases, pain and infectious disease.
XX
SQ Sequence 2535 BP; 549 A; 725 C; 688 G; 573 T; 0 other;

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Query Match 22.6%; Score 569.4; DB 20; Length 2535;
Best Local Similarity 54.8%; Pred. No. 4e-170;
Matches 1231; Conservative 0; Mismatches 981; Indels 33; Gaps 4;

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QY 130 ccatgagccgcaaaaggagatggcagggcgccagcggtgtgtatgctgcgcacaaagactg 189
Db 172 ctgtttcccatgagcgggggtgcccaggggcccagggcctgcagcccggtggagatg 231
QY 190 gogttggatgatgcacaagcagcgaatctgtcgcggggttcgaagctcactcctgcac 249
Db 232 gcgctggaggacgtgaatagccgagggacatctgcggactatgagctcaagctcatc 291
QY 250 agcaacgacagcagtgtagcccggtttggcgccagcgtgtagtataaatctgcttat 309
Db 292 caccagcagcagtgtagccagggcccaagcccaagttacctatatagctgtgctctac 351
QY 310 aataaacccgcaaaagctgtgtgtggcaggtgagcagcagcgtctgtcacactgtagcc 369
Db 352 aacgacctatacaagatcatcttatgctgctgagctctgtctccacgctgggtgct 411
QY 370 gaggtgcccataatgtggaatctaatgtgtctgtctacggggcctcagtcgcggtctt 429
Db 412 gaggtgctaggtgtggaacctcattgtgtcttctctatggtgccagctcaccagccgtg 471
QY 430 tggatgcgaacagattccccactctattccgcaccatccatccatggcagcgggtgcacaat 489
Db 472 tcaaacggcgagcgttcccccacttcttcgcaagcaccatccagcagcactcccaaac 531
QY 490 ccaacgcgcatcaagctgatgaagaattcgctggtcccggtggccattcttcgacgag 549
Db 532 cctaccgcgctgaaactcttgaaggggggtggaagattgtaccatccagcag 591
QY 550 ggggagggaggtctttatatcgaccgtagaggtatctcgagaatcgatgcatggaggtggc 609
Db 592 accatgaggtcttctactctgactctgagcagctggaagaaagtgagagggctgga 651
QY 610 gttgaaatcgtaactagacaaatcatttctatccgatacccaacagcgcgtgcgcaattg 669
Db 652 attgagattactttccgcagagatttctctcagatccagctgtgccgtcaaaaaacctg 711
QY 670 cgacgcagagatgcagcatcattgtgggactctctctatgtgtgcccagaggggtg 729
Db 712 aagcgcagagatgcccgaatcactcggggacttctctatgagactgaagcccggaaagt 771
QY 730 ctctcgaaaatgtacaaacagcagctatatggcgcagctcatgtgtgtttctttattggc 789
Db 772 tttgtgaggtgtacaaggagcgtctctttgggaagaagtacgtctgttctcattggg 831
QY 790 tggtagaggaacaactggttacgaggtgaaatctgaaagcagagagggcactcactgactgtt 849
Db 832 tggtagtgacaaattggt-----tcaagatctacgaccttctatcaactgcacagt 885
QY 850 gaacagatcggaatagctccggaagagacatctgacaaagggaagcgtcatgtggaatcag 909
Db 886 gatgagactgactgagcgggtggagggccacatcacaaactgagattgtcgtggaatcct 945
QY 910 aacaatcacacaactatataccggaatgactgcagagaaatttcgacatcgactgaatcag 969
Db 946 gccaataccgcgagcatttcccaatgacatcccaggaaatttggagaaactaaccaag 1005
QY 970 gcgctaactgagaggggttacgacatttaaacacgactcgctatccggaggagatatcaggag 1029

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Db 1006 cgactgaaagacacccctgaggaga-----caggaggcttccaggag 1047
QY 1030 gcgcactcgcctacgacgagtgagtgagtggtggttgccttcaacaagaccatggaa 1089
Db 1048 gcaacgctggcctatgacatctggcccttggcactggccctgaaacaagacatctgga 1107
QY 1090 cgattgacaaccgggaagaaatctctgaggatatttaacctatacaggaagagattgcc 1149
Db 1108 ggaggcgccgttctgtgtgcctggaggaacttcaactcaacaacacagaccattacc 1167
QY 1150 gatgaatctacgctgcctgaactccacacaattctcgggtgtatcgggtgtgtgggca 1209
Db 1168 gaccaaatctaccgggcaatgaactcttgccttggagggtgtctcggccatgtggtg 1227
QY 1210 ttcaagttcagggcgatctgtattgtcttatacacagatcgacagatgatagacggcaag 1269
Db 1228 ttgatgccagcggtctcggatggatggacgttatacgagcagcttcaagggtggcagc 1287
QY 1270 tacgagaagttgggttactacgatactcagttgataacctatctcgttgaataactgaa 1329
Db 1288 tacaagagattggctactatgacagcaccagagatgatcttctcgtgtccaaacagat 1347
QY 1330 cagtggattggtggcaagggttctcgaagtcgcacaattgtcaacctgttctacgcacc 1389
Db 1348 aaatggattggagggttccccccagctgacagaccctgggtcatcaaacatccgccttc 1407
QY 1390 gtgtccttgcattattgtgtgcatgtgcacaatatccagttgtgggcatattcgttgc 1449
Db 1408 ctgtcacagaaactcttatctcgtctcagttctctccagcctggcattgtcttagct 1467
QY 1450 ttgccttgatcatctttaatatatggaataagaatagaagaataatacaatcctcgcgt 1509
Db 1468 gttgtctgtctgtcttaacatctacaactcacatgcctgttcttatccagaactcacag 1527
QY 1510 cccgtttgcaatcagatcatgtattgtgtgtcatctcgtctcaatatctgtcatctta 1569
Db 1528 cccaacctgaacaacctgactgctgtgtgggtgtcactgtgttagctgtgtcttcccc 1587
QY 1570 ctgggcatcgacgacgcttctgtcagcccgagggaataatccaaagatatgtcaagcgcg 1629
Db 1588 ctggggctcgatggttaccacatgggagggaaccaggttctcttctgtcgcaggccgcg 1647
QY 1630 gcttggttactatccacggttttaactatgatacagtgctatgttccagcaagctcgtg 1689
Db 1648 ctctggctctcgtcgtggctgttagtctgtggtctacggttccatgttccaccaagattgg 1707
QY 1690 cgtgtgcatgcttttacaaca-----aaqcaaaaactgcccaaaaagaaagtga 1743
Db 1708 tgggtccacagcgtcttccaaaagaagaagaagaagggagtgagggaagactctgaa 1767
QY 1744 ccttggagctatacacccatggttctcgggctattatcaatagatttagtgatattactc 1803
Db 1768 ccttggagctgtatgccacagtggtcgtggtggcagtgatgtctcactctcgc 1827
QY 1804 tcatggcagatcttctgcctcgtcagcgttatctcgaacacattccccactcgaagatcca 1863
Db 1828 atctggcagatcgtggaccctctgcacggaccattgagacatttgccaaggaggaacct 1887
QY 1864 gtatctactactgatataataaatacgtccagagcttgagcattgtgaaagtcaacgc 1923
Db 1888 aaggaagatattgacg---tctctatctcgccccagctggagcattgcagctccaggag 1944
QY 1924 aactccatgtgtgtgtgtctgtatcagcgttccagggttaactcctggttctggccctc 1983
Db 1945 atgaatacatggttggcattttctatggtttacaagggtcgtcgtcgtcgtcgtgggaatc 2004
QY 1984 tttttggctacgagacgcctccattaaagtgaacagatcaacgactcagcgttctgtatgtg 2043
Db 2005 ttctcgttattgagaccagaagtggttccactgagaagatcaatgatcaccgggctgtg 2064
QY 2044 ggcatgacatcataacgttggtgtcgttcttgcctgataacagctcccggtgggcatggtc 2103
Db 2065 ggcattgctatcataatgtggcagtcctgtgctcctcatcactgtcctcgtcaccatgatt 2124
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QY 2104 attgcatacgcaacagcagcgctcttgccttgccttgccttagctgtgatatctgtgtg 2163
Db 2125 ctgtccagcagcagcagcagcagccttgccttgccttgccttagctgtgatatctgtgtc 2184
QY 2164 ttctaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2223
Db 2185 tatatacctcttgccttgccttgccttgccttgccttgccttgccttgccttgccttgc 2244
QY 2224 gataagcgcgaatcgaatacaatacccgattccagccatcgaagaggagcagaagacgc 2283
Db 2245 tggcagtcggagcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2304
QY 2284 tatcagaaaactgttaccgaaaacagcgaattgcacagcagcagcagcagcagcagcag 2343
Db 2305 gagaagctccggtgtgttgagaaggagacccgtgaactggaaaagatcattgctgagaaa 2364
QY 2344 aagattcgagctcgcagcagcgtc 2368
Db 2365 gaggagcgtgtctcgaactgcgc 2389

RESULT 5
AA58067
ID AAX58067 standard; cDNA to mRNA; 2602 BP.
XX
AC AAX58067;
XX
DT 21-JUL-1999 (first entry)
XX
DE Human GABAB receptor lj coding sequence.
XX
KW GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;
KW transient lower oesophageal sphincter relaxation; spasticity; emesis;
KW gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;
KW irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;
KW autoimmune disease; neoplastic disease; infectious disease; therapy;
KW alternative splicing; isoform; ss.
XX
OS Homo sapiens.
XX
PN W09921890-A1.
XX
PD 06-MAY-1999.
XX
PF 27-OCT-1998; 98MO-SE01947.
XX
PR 17-JUL-1998; 98SE-0002575.
PR 27-OCT-1997; 97SE-0003914.
PR 16-MAR-1998; 98SE-0000864.
XX
PA (ASTR ) ASTRA AB.
PI Ekstrand J;
XX
DR WPI; 1999-302985/25.
DR P-PSDB; AAY14112.
XX
PT Polynucleotides encoding human and canine gamma aminobutyric acid
PT type B receptors, used to screen for compounds that are inhibitors
PT of transient lower oesophageal sphincter relaxations
XX
PS Example 7; Page 203-205; 222pp; English.
XX
CC This sequence encodes an isoform of a human gamma aminobutyric acid
CC type B (GABAB) receptor of the invention, created by alternate splicing.
CC Nucleic acid molecules encoding GABAB receptors can be used to screen for
CC compounds that are inhibitors of transient lower oesophageal sphincter
CC relaxations (TLESR). They can also be used to screen for agonists or
CC antagonists of the GABAB receptors. Inhibitors of TLESR are useful for
CC treating gastro-oesophageal reflux disease. Other uses of GABAB
CC receptors, such as human GABAB Rlc or ld, comprise diagnosis or treatment
CC of conditions related to GABAB dysfunction, e.g. epilepsy, psychiatric
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CC disorders, emesis, irritable bowel syndrome, dyspepsia, spasticity,
CC arthritis, allergies, autoimmune diseases, neoplastic diseases, pain and
CC infectious disease.
XX
SQ Sequence 2602 BP; 582 A; 737 C; 702 G; 581 T; 0 other;

Query Match 22.68; Score 569.4; DB 20; Length 2602;
Best Local Similarity 54.8%; Pred. No. 4e-170;
Matches 1231; Conservative 0; Mismatches 981; Indels 33; Gaps 4;

QY	130	ccgatagccgcaagagagatgcagcggcgccagcgctgtatccctgccacaagactg	189	1115	gcaccgctggccctatgatgccatctctgggccccttgccactggccctgaacaagacatctgga	1174
DB	239	ctgtttcccatgagcgggggctggcaggggccaggccctgccagccgcgggtggagatg	298	1090	cgattgacaacccgggaagaatactctgagggattttaccctatcacggacagagatggcc	1149
QY	190	gcgttgatgatgtcaacaagcagccgaatctgtcgcggggttcaagctcatcctgcac	249	1175	ggagcgccgcttctggtgtgcccggaggacttcaactacaacaacagaccattacc	1234
DB	299	gcgctggagcgtgaatgcgcagagacatctcgcgactatgagctcaagctcatc	358	1150	gatgaatactacgctgccatgaaactccacaataattctgggtgtatcggtgtggtggca	1209
QY	250	agcaacgacagcagtgtagcccggtttggcgccagcgtgatgtacaatctgctctat	309	1235	gaccaactctaccgggcaatgaactcttctctttgaggggtctctgcccattgtgtg	1294
DB	359	caccacgacagcaagtgtgaccaggccaaagcccaagctacattatgagctgcttac	418	1210	ttcagttctcagcgcatgattgtctcttacagatcgaaacagatgatagacgcgaag	1269
QY	310	aataaacgcaaaagctgactgtttggcaggatgcagacaggtctgcaccactgtagcc	369	1295	tttgatgcagcggtcctcgatggcatggacgttatcgagcagcttcaggggtcggcagc	1354
DB	419	aacgacctatcaagatcatcttatgctgctgagctgtgtctccacgctgtggt	478	1270	tacgaagaattgggttactacgatactcagttggataacctatcctggttgaatactgaa	1329
QY	370	gaggtgccaaaattggaattctaatgtgctctgacgggctcgagtcgagtcgctctt	429	1355	tacaagaagtggctactatgacagcacaagatgatcttctcgtgtccaaacagat	1414
DB	479	gaggtctctagatgtggaacctcatgtgtttctctatggctccagctcaccccttg	538	1330	cagtgattggtggtgcaaggttcctcaagatcgcaaatgtgcacccattgttctacgacc	1389
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QY	490	ccaacgcgcatcaagctgatagaataatcggtggtccccgggtggccattctgcagcg	549	1475	ctgtcacaaaactcttatactcgtctcagttctctccagcctggcatgttctctagct	1534
DB	599	ctcaccgcgtgaaactctttgaaaagtgggctggaagaagattgctaccatccagcag	658	1450	ttcgcttgatcatctttaatatatggaataagcataagaagaagtaatacaatccctgcac	1509
QY	550	gcggagaggtctttatcagccgtagagatctcagaaatcagatcgatgagactgac	609	1535	gttgtctgtctgtccittaaactctacaactcacatgcogttatacceagaactccag	1594
DB	659	accaactgaggtcttcaactcagctcgacacccctggaggaaagtgtaagggctgga	718	1510	cccgtttgcaatacagcatctgtattgttggtgtcatcatctgtctaatatctctcatctta	1569
QY	610	gttgaatatgtaactagacaatctttctatccgatcccaacagacgcgtgcgaatttg	669	1595	cccaactgaacaacctgactgctgtgggctgtctcactgctttagctgtctgtctcccc	1654
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QY	670	cgacgcaggatgcagcgcattgttgggaactctctctatgtgtggtggccgcaggggctg	729	1655	ctgggctcgatggttaccacattggaggaaacagtttctctctcgtccagggccgc	1714
DB	779	aagcgcaggatgcgcgaatcatcgtggacttttctatgagactgaagcccggaagt	838	1630	gctgtgtactatccaccggttttacactagcatcagctgctatgttcacgaaggtctgg	1689
QY	730	ctctgcgaatgtacaacagcagctatattgccgcagctcatgtgtgtttttattggc	789	1715	ctcgtgctcctggcctgggtttagtctggttcacggttccatgttccacaagatttgg	1774
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QY	790	tgggtacgaggacaactgggtacaggtgaaatctgaaagcagagggcatcacctgcactgtt	849	1775	tgggtccacacgcttctcaacaagaaggaagaaagaggtggaggaaagactctggaa	1834
DB	899	tgggtactgcaattggt-----tcaagatctacgaccttctatcaactgcacagt	952	1744	cttggaaagctatacaccatggtttcgggctattatcaatagatttagtgatatctac	1803
QY	850	gaacagatgcgaatagctgcgaaggacatctgcacaacggaagcgtcatgttggaaatcag	909	1835	ccctggaagctgtatgccacagtgggcctgctgtgtgggcatggatgtcctcactctgc	1894
DB	953	gatgagatgactgagcgggtgagggccacatcacaactcagatgtgatgtgctgaatct	1012	1804	tcattgcagatcttgcacgcgtgcagcgttatctcgaaacattcccactcgaaagatcca	1863
QY	910	aacatcagacaactatctcgggaatgactgcagagggaatttcgacatgcactgaatcag	969	1895	atctggcagatcgtggaccctctgcacggacacattgagacatttgcgaaggaggaacct	1954
DB	1013	gccaatccccgcagacttccaacatgacatccccaggaatttgtggaaacactaaccag	1072	1864	gtatctactactgatgatattaaaatacgtccagagcttgagcattgtgaaagtcaacgc	1923
QY	970	gcgctaactcgagggggttacgacattaaaccacgactctatcccgagggatcatcagag	1029	1955	aaggaagatattgacg---tctctattctgccacgctggagcattgcagctccaggag	2011
DB	1073	cgactgaaaagacacctgagaga-----caggagggttccaggag	1114	1924	aactccatgtggttgggtctgtatagcgttcaaggggctaatcctcgtgttctggcctc	1983
QY	1030	gcgccaactcgctacgtacgtgtagtgagggtggcctttggctttgaccttcaacaagaccatggaa	1089	2012	atgaatcacatggcttggcatttctatgggtacaaggggctgctgctgctggggaatc	2071
DB				1984	ttttggcgtacgagacgcgctccattaaagtgaacagatcacgattccgcttatgtg	2043
				2072	ttccttgccttatgagaccaagagtgtgtccactgagaaatgatcatcccgccgctgtg	2131
				2044	ggcatgagcatctatacgtgtgtcgtcttctgctgataaacagctcggtgggcatggct	2103
				2132	ggcatggctatctacaatgtggcagtcctgtgcctcactgctcctgtccacatgatt	2191
				2104	attgcatcgcaacagcagcgtcctttgcttctgtctctagctgtgatattctgtgt	2163
				2192	ctgtccagccagcagatgcagccttggccttctgtcctctcttgccatagtttctctcc	2251

Qy	2164	ttcctaagcatgctgctgtatatttgccaaaggctcattgaggttatcatcgtcatcccaag	2223		
Db	2252	tatatcactctgtgtgctcttttggccaaagatcgaggtgatcaccgaggggaa	2311		
Qy	2224	gataaggccgaatcgaataacaatcccgtattcagccatctcgaagaggacgaagaacgc	2283		
Db	2312	tgccagtcgagcgagcaccatgaagacagggtcatcgaccacaacaacacgaggag	2371		
Qy	2284	tatcagaactgttaccgaaacagcaattgcaacgatttaataacacagaagaggaa	2343		
Db	2372	gagaagtcgccgcttggagagaggaaccgtgaactggaagaagatcattgctgagaaa	2431		
Qy	2344	aagattcgagtcctgcagacgcgc	2368		
Db	2432	gaggagcgtgctctgaaactgcgc	2456		
RESULT 6					
AAV10265	AAV10265 standard; cDNA to mRNA; 2620 BP.				
XX	AC	AAV10265;			
XX	AC				
DT	03-JUN-1998	(first entry)			
XX	Human GABA-BR1a/b receptor cDNA.				
XX	Gamma-aminobutyric acid; GABA-BR1a/b receptor; human; brain; agonist;				
KW	inhibitory neurotransmitter; peripheral nervous system; antagonist;				
KW	treatment; dementia; depression; anxiety; bronchial inflammation; asthma;				
KW	epilepsy; cognitive function; ds.				
XX					
OS	Homo sapiens.				
XX					
EH	Key	Location/Qualifiers			
FT	CDS	1..2382			
FT	/*tag= a				
FT	/product= GABA-br1a/b				
XX					
PN	W09746675-A1.				
XX					
PD	11-DEC-1997.				
XX					
PF	19-MAR-1997;	97WO-EP01370.			
XX					
PR	22-NOV-1996;	96US-0756091.			
PR	30-MAY-1996;	96US-0655716.			
XX					
PA	(NOVS) NOVARTIS AG.				
XX					
PI	Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;				
XX					
DR	WPI; 1998-042183/04.				
DR	P-PSDB; AAW40117.				
XX					
PT	Purified GABA-B receptor or receptor protein - and antagonists of				
PT	these which may be useful in treating nervous system disorders				
XX					
PS	Claim 3; Page 56-62; 108pp; English.				
XX					
CC	This cDNA sequence encodes a novel human GABA-B receptor protein,				
CC	GABA-BR1a/b. GABA (gamma-aminobutyric acid) is the major inhibitory				
CC	neurotransmitter found in the brain and peripheral nervous system				
CC	and this receptor may be used for the identification of GABA-B				
CC	receptor agonists and antagonists. Such proteins may be used in				
CC	treatment of dementia, depression, anxiety, epilepsy, spasticity,				
CC	bronchial inflammation or asthma or to improve cognitive function.				
CC	GABA-B receptor ligands and probes derived from this sequence can be				
CC	used to assay for GABA-B receptors or DNA encoding them.				
XX					
QQ	Sequence 2620 BP; 593 A; 716 C; 710 G; 601 T; 0 other;				

Query Match				22.6%	Score 569.4	DB 19	Length 2620
Best Local Similarity				54.8%	Pred. No. 4e-170		
Matches 1231				Conservative	0	Mismatches 981	Indels 33
QY	130	ccgatagccggc	caagaggagatg	gcaggcgccg	gcaggcggtgatg	cctgccacaagactg	189
DB	19	ctgtttcccat	tgagcggggctg	gccaggggccg	ggcaggcctgccagcccg	gggtggagatg	78
QY	190	gcgttgatgatg	tcaacaagcagc	cgaaatctg	ctgccgggctccaagctcatcctgcac	249	
DB	79	gcgctggagacg	tgaatagccg	cagggacac	ctcctgccggactatgagctcaagctcatc	138	
QY	250	agcaacgacg	cagtgatgagcccg	gtttgggcgcacg	tgatgtacaaatctgtctcat	309	
DB	139	caccacgacg	caagtgtgatccag	gccagccacaa	ctaatctatgagctgctctac	198	
QY	310	aataaacgcg	caaaagctgagtctg	tgtggcaggatgcag	cagcgtctgcaccactgtagcc	369	
DB	199	aacgacctat	tcaagatcatctctat	gctgctggctgcagctctctccacgctg	tggtg	258	
QY	370	gagcctgc	caaaatgtggaatc	taattgtctctgc	tacgggcccctgcgagtc	gcgtctt	429
DB	259	gagcgtctag	gaagtgggaacctca	tgtgctttctatggctccagct	caccagccctg	318	
QY	430	tcgcatcg	caaacgatctccca	ctctatctgcg	caccatccatcgcgcacg	ctgcacat	489
DB	319	tcaaacgcg	cagcgtttcccca	ctttctccgaacgc	acccatcagccacactccacaac	378	
QY	490	ccaacgcgc	atcgaagctgatga	agaaatctcg	gtgtcccgggtggccatctctgcagcag	549	
DB	379	ctcacccgcg	tgaacctcttgaa	agtgggctggaagagattg	ctacccatccagcag	438	
QY	550	gcgagagag	gtctttatcg	acogtagagatctcg	agaatcgatgcagtgagcgtcgc	609	
DB	439	accactgag	gtctccactgtgcg	actgtggagcagcgtggaagc	gagtgagggctgtga	498	
QY	610	gttgaatc	gttaactagaca	atcttctatccgat	ccacaagacgcgcgtgcgcaattg	669	
DB	499	attgagatt	actttccgcagag	tttctctcagatcc	agctgtgccctcaaaaacctg	558	
QY	670	cgagccagga	tgcacgcata	ctatgtgtgggactctctat	gtgtgtgcccgcgcaggagggtg	729	
DB	559	aagcgcagga	tgcgcgaatctcat	gtggactttctatgagact	gaagccgcggaaagt	618	
QY	730	ctctgc	caaatgttaca	aacagcagctata	tggccgagctcatgtgtgtttctttatg	789	
DB	619	tttgtgag	gtgtacagaggc	gtctcttttgggaagaag	tacgtctcgtgttcttcatctgg	678	
QY	790	tgttacgag	gacaactggtac	gagtggaatctg	aaaagcagagggcactcacctgcactgtt	849	
DB	679	tggatgct	gacaattggt	-----tcaagat	ctagacccctctatcaactgcacagtg	732	
QY	850	gaacagat	gcgaatagctgcg	gaaggacatctg	acaacgcgaaagcgtctatgttggatcag	909	
DB	733	gatgagat	gactgagcgg	tggaggccacatcaca	actgagattgtcatgtgctaact	792	
QY	910	aacaatcag	acaactat	atccggaatgactgc	agaggaatttcgacatcgactgaatcag	969	
DB	793	gccaatcc	gcgacgat	ttcccaatgacatcc	cagggaatttgggagaaactaaccaag	852	
QY	970	gcgttaat	cgaggagggttac	gacattaa	ccgcgctatccggagggatcatcagag	1021	
DB	853	cgactga	aaagacac	ccctgaggga	-----caggaggcttccaggag	894	
QY	1030	gcgcactc	gcctacgactg	agtgtagtg	tggtcttgccttcaacaagaccatggaa	1081	
DB	895	gcacgcgt	gccttatgatgc	atctggtcct	tggtcagcgtgcacagacatctgga	954	
QY	1090	cgaatg	caaacccggg	gaagaaatctctg	agggatttacctctatcagcaagagattg	1141	
DB	955	qgaagc	gccttctgtgtgt	ctgcctctgaagccttca	actcaacacacagacacattac	1011	


```
Db 2449 gagaagtcctggctgttgagagagagaaacctgtaactggaaagatactattgctgagaaa 2508
Qy 2344 aagattcagtcctgcgcagcgtc 2368
Db 2509 gaggagcgtgtctctgaactgcgc 2533

RESULT
AAX58062
ID AAX58062 standard; cDNA to mRNA; 2700 BP.
XX AC
XX AAX58062;
DE 21-JUL-1999 (first entry)
DE Human GABAB receptor 1e coding sequence.
XX KW
XX GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;
XX transient lower oesophageal sphincter relaxation; spasticity; emesis;
XX gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;
XX irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;
XX autoimmune disease; neoplastic disease; infectious disease; therapy;
XX alternative splicing; isoform; ss.
XX OS
XX Homo sapiens.
XX PN
XX WO9921890-A1.
XX PD
XX 06-MAY-1999.
XX PF
XX 27-OCT-1998; 98WO-SE01947.
XX PR
XX 17-JUL-1998; 98SE-0002575.
XX 27-OCT-1997; 97SE-0003914.
XX 16-MAR-1998; 98SE-0000864.
XX PA
XX (ASTR ) ASTRA AB.
XX XX
XX Ekstrand J;
DR WPI: 1999-302985/25.
DR P-PSDB: AAY14107.
XX
XX Polynucleotides encoding human and canine gamma aminobutyric acid
XX type B receptors, used to screen for compounds that are inhibitors
XX of transient lower oesophageal sphincter relaxations
XX
XX Example 7; Page 162-168; 222pp; English.
XX
XX This sequence encodes an isoform of a human gamma aminobutyric acid
XX type B (GABAB) receptor of the invention, created by alternate splicing.
XX Nucleic acid molecules encoding GABAB receptors can be used to screen for
XX compounds that are inhibitors of transient lower oesophageal sphincter
XX relaxations (TLESR). They can also be used to screen for agonists or
XX antagonists of the GABAB receptors. Inhibitors of TLESR are useful for
XX treating gastro-oesophageal reflux disease. Other uses of GABAB
XX receptors, such as human GABAB R1c or 1d, comprise diagnosis or treatment
XX of conditions related to GABAB dysfunction, e.g. epilepsy, psychiatric
XX disorders, emesis, irritable bowel syndrome, dyspepsia, spasticity,
XX arthritis, allergies, autoimmune diseases, neoplastic diseases, pain and
XX infectious disease.
XX
XX Sequence 2700 BP; 599 A; 764 C; 741 G; 596 T; 0 other;
XX SQ

Query Match 22.6%; Score 569.4; DB 20; Length 2700;
Best Local Similarity 54.8%; Pred. No. 4.1e-170;
Matches 1231; Conservative 0; Mismatches 981; Indels 33; Gaps 4;

Qy 130 ccgatagccgcaaggaggatggcaggggccaggcggctgtatgcctgcccaagactg 189
Dp 337 ctgtttcccatgagcgggggctggccaggggggccaggcctgccagcccggtggagatg 396
```

```
Qy 190 gccttgatgatgtcaaaagcagccgaaattgtctgccgggtcttaagctcatcctgcac 249
Dp 397 gcgctggaggagcgtgaatagccgcgaggacatcctgcgactatgactcaagctcatc 456
Qy 250 agcaaacgacagcagtgatgagcccggtttgggcgcagcgtgatgtacaattctctctat 309
Dp 457 caccacgacagcaagtgtgatccaggccaagcccaagtaacctatgatgtctctac 516
Qy 310 aataaacccgcaaaagctgctgttgccaggtgagcagcagcgtctcaccactgtagcc 369
Dp 517 aacgacctatcaagatacctctatgcctggctgagctctgtctccacgctgtggct 576
Qy 370 gaggtgccaaaatgttggaattgtctctgtctacggggcgtgagtcgggctctt 429
Dp 577 gaggtgctaggtgtggaacctcattgtgtcttctatggctccagctcaccagccctg 636
Qy 430 tcggatcgaaacgattcccaactctattccgacccatccatcggccagcaggtgcacaaat 489
Dp 637 tcaaacggcagcgtttcccaactttctccgaacgacccatcagccacactcacaac 696
Qy 490 ccaacgcgcacatcaagctgatgaagaattcggctgggtcccggtggtcattcttcagcag 549
Dp 697 cttaccgcgtgaacctctttgaaaagtggggctgggaagattgtctacatccagcag 756
Qy 550 gcggaggaggtcttttatcgaccgtgaggtatctcgagaatcgatcgatggagcgtggc 609
Dp 757 accactgaggtcttctcacttcgactcgacgacctgaggaacgagtgaaaggagctgga 816
Qy 610 gtgaaatcgtaactagacaaatattctatccgatccacacagacgcgcgtgcgcaatttg 669
Dp 817 attgagattactttccgccagagttttctcagatcagcgtgtgcccacaaacctg 876
Qy 670 cgagccaggtgcacacatcattgtggactcttctatgtgtggcgccgagaggtg 729
Dp 877 aagcgcaggatgcccgaaatcactcgtggactttctatgagactgaagccgggaaagt 936
Qy 730 ctctcgaaaatgtacaaacagcagctatatggccgagctcatgtgtgtgtttttattggc 789
Dp 937 tttgtgaggtgtacaaggagcgtctcttgggaagtaagtaactgtgttctcatggg 996
Qy 790 tggtaggaggaacactggtacgaggtgaatctgaaagcagagggcaccatccactgactgtt 849
Dp 997 tggtagtgtacaaattggt-----tcaagatctacgaccttctatcaactgacagt 1050
Qy 850 gaacagatcgaaatagctgcggaagacatctgacacgaaagcgctcatgtgaaatcag 909
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Dp 1111 gccaataccgcagcatttccaaatgacatcccgagaatttgggaaactaaccaag 1170
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Dp 1171 cgactgaaagacacctgaggaga-----caggagggttccaggag 1212
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Dp 1273 ggaggcggcgttctgtgtgctgaggtgaggttcaactaacacacacacacacacacacac 1332
Qy 1150 gatgaattctacgtgccatgaaactccacaaatttctgggtgtatcggtgtgtgtgtgtgtgt 1209
Dp 1333 gaccaaatctaccgggcaatgaaactcttctgcttgggggtgtctctggcctatgtgtgt 1392
Qy 1210 ttcagttctcagggcagtcgtattgtctcttacacagatcgaacacagatgatagacggcaag 1269
Dp 1393 ttgatgccagcggctcctcgatggcatggagcgttatcgagcagcttcaagggtggcagc 1452
```

QY	1270	tacgagaagttggtttactacagatactcaagtgtggatacaacctatctcctggttgaatactgaa	1320
Db	1453	tacaagaagattggctactatgacagcaccagaagtgtctttcttctggtccaaaaagat	1512
QY	1330	cagtggattggtggcaaggttctccaagatcgacacaattgtcaacctatgtcttacgcacc	1389
Db	1513	aaatggattggagggttccccccagctgaccagacctgtctatcagaacatttccccttc	1572
QY	1390	gtgtccttgccattatttgtgtgcattgtgcacaataccagttgtggtgcattatcgttgcc	1449
Db	1573	ctgtcacagaacctttatctccgtctcagttctctccagctggccatgttctctagct	1632
QY	1450	tctgccttgatcatctttaaataatggaaatagcatagaagagtaatacaaatctctcgcat	1509
Db	1633	gtgtctgtctgtctttaacatctacaactcacatgtccgttatataccagaactcacag	1692
QY	1510	ccggttgcatacagatcatgttatttgggtgctcatcatctgtctctaatactgtctcatctta	1569
Db	1693	cccaacttgaaacaactgactgctgtgggtgctgctcactggcttttagctgtcttctccc	1752
QY	1570	ctgggcatcgagcagcgttttgcagccccggaggaaatattccaaaagatattgtcaagcgcgg	1629
Db	1753	ctggggtctgattggttacacaattggggaggaccaggtttctcttgcctgcagggcccgc	1812
QY	1630	gcttgggttactatcacocgggttttacactagatcatcaggtgctatgttccagcaaggtctgg	1689
Db	1813	ctctgggtccctgggcctgggtttagtctctgggtcaggttccatgttccacaagatttgg	1872
QY	1690	cgtgtgcatcgtttttacaaaacaa-----aagcaaaaactgaccccaagaaaaagtgaaa	1743
Db	1873	tgggtccacacgcgtcttcacaaaagaaggaagaaaagaagaggtggaggagaactctggaa	1932
QY	1744	ccttggaaactatcacacatagtttctggggctattatcaatagatttagtattacttctc	1803
Db	1933	cccttgggaagctgtatggccagctggggcctgtgtggggcatggatgtctctcactctgcgc	1992
QY	1804	tcatggcagatcttttgatccgctgcagcgtttatctctgaaacattcccatcgaagatcca	1863
Db	1993	atcttggcagatcggtggaccctctgcacgcgaccattgagacatttgcgaaggaggaaacct	2052
QY	1864	gtatctactactgatgatattaaaatacgtccagagcttgagcattgtgaaagtcacacgc	1923
Db	2053	aaggaagatataggc---tctctattctgccccagctggagcatttgcagctccaggaaag	2109
QY	1924	aactccatgtggttgggtcttgtatcacgcttcgaaggctcaagggtctaactcctgtgttgcctc	1983
Db	2110	atgaatacatggcttggcattttctatggtttacaaggggctgctgctgctgtctgctgggaatc	2169
QY	1984	tttttggcgtacgagacgcgtccattaaaagtgaacagatcaacagattcgcggttatgtg	2043
Db	2170	tctctgttatgagaccagaagtggtctccactggagaagatcaatgatcacccgggtctgtg	2229
QY	2044	ggcatgagcatctataaagtggtgcgtctcttggcctgataaacagctccggttgggcattgctc	2103
Db	2230	ggcatggtctatcaaatgtggcagctgctgtgcctcaactgcactgctgctgtccacatgatt	2289
QY	2104	attgcattcgaaacagcgcgtcttggccttgcgttgccttagctgtgattattctgttgt	2163
Db	2290	ctgtccagcagcaggatgcagcctttgcttcttgcctctcttgcacataglttttctcctcc	2349
QY	2164	ttcttaagcatgctgctgatatttggccaaaggtcatttgaggtttatacgtcatcccaag	2223
Db	2350	tatatcactctgtgtgctctttgtgtgccaaagtgcgcaggctgatcacccgaggggaa	2409
QY	2224	gataagccggaatcgaaaatacaatcccgattcagccatatcgaaagagaggacgaagaacgc	2283
Db	2410	tggcagctcgaggcgcaggaccacatgaagacaggggtctatcgaccacaacacacagggag	2469
QY	2284	tatcagaacctgttacggaaaaacgcgcaattgtcaacgttaataaacacagaagaggaa	2343
Db	2470	gagaagtcctcggtctgttggagaaggggaaccgtagactggaaaagatcatctgtgagaa	2529
QY	2344	aagattcgagtcctgcgacagcgtc	2368

Db 2530 gaggaggtgtctctgaactgcgc 2554
 || || ||| || ||| |
 RESULT 9
 AAZ35410
 ID AAZ35410 standard; cDNA; 2822 BP.
 XX
 AC AAZ35410;
 XX
 DT 27-MAR-2000 (first entry)
 XX
 DE Human G-protein coupled receptor GABAB1b cDNA.
 XX
 KW GABAB1b; G-protein coupled receptor; human; antibacterial;
 KW antiviral; virucide; antiparasitic; analgesic; cytostatic;
 KW antididiabetic; anorectic; cardiant; antiparkinsonian;
 KW hypertensive; hypotensive; antiemetic; osteopathic; antianginal;
 KW cerebroprotective; antiulcer; antiallergic; neuroleptic;
 KW tranquilizer; antidepressant; nootropic; antimigraine;
 KW anticonvulsant; neuroleptic; agonist; antagonist; inhibitor;
 KW therapy; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 49..2583
 FT /*tag= a
 FT
 XX
 PN W0995958567-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 03-MAY-1999; 99WO-US09655.
 XX
 PR 08-MAY-1998; 98US-0075463.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Elshourbagy NA, Halsey WS;
 XX
 DR WPI: 2000-116287/10.
 DR P-PSDB; AAY32467.
 XX
 PT New human GABAB1b polypeptides and polynucleotides used to identify
 PT agonists, antagonists and inhibitors for use in therapy -
 XX
 PS Claim 2; Page 33-35; 46pp; English.
 XX
 CC This is the nucleotide sequence of human cDNA coding for the
 CC G-protein coupled receptor GABAB1b (see AAY32456). The cDNA was
 CC obtained by PCR amplification (see AAZ35411-12) using brain cDNA as
 CC template. The invention provides GABAB1b polypeptides and
 CC polynucleotides, and methods for producing such polypeptides by
 CC recombinant methods. GABAB1b polypeptides may be used for
 CC identifying agonists and antagonists/inhibitors, and for detecting
 CC diseases associated with inappropriate GABAB1b activity or levels.
 CC GABAB1b polypeptides and polynucleotides, agonists, antagonists and
 CC antibodies are used to treat bacterial, fungal, protozoan and viral
 CC infections, particularly HIV-1 and HIV-2, pain, cancer, diabetes,
 CC obesity, anorexia, bulimia, asthma, Parkinson's disease, acute
 CC heart failure, hypotension, hypertension, urinary retention,
 CC osteoporosis, angina pectoris, myocardial infarction, stroke,
 CC ulcers, allergies, benign prostatic hypertrophy, migraine,
 CC vomiting, psychotic and neurological disorders including anxiety,
 CC schizophrenia, manic depression, depression, delirium, dementia and
 CC severe mental retardation, and dyskinesias such as Huntington's or
 CC Gilles de la Tourette's syndrome. The polynucleotide is also
 CC useful as a source of primers and probes, and for detecting the
 CC above diseases.
 XX
 SQ Sequence 2822 BP; 612 A; 820 C; 760 G; 630 T; 0 other.

22		gaggggtcccccgcctcctcgacagcgtc	2368
QY	2344	aagattcgagtccctgcgacagcgtc	2368

Query Match 22.6%; Score 569.4; DB 21; Length 2822;
Best Local Similarity 54.8%; Pred. No. 4.2e-170;
Matches 1231; Conservative 0; Mismatches 981; Indels 33; Gaps 4;

QY	130	ccgatagccggaagagagatgagcagcgccgagcggtgtatccctgccacaagactg	189	1150	gatgaaatctacgctgccatgaaactccacacaaatttctgggtgtatcggtgtgtgtgga	1209	
DB	220	ctgtttcccatgagcggggctggcagggggcccgagcggtgcagcccggtggagatg	279	DB	1216	gacaaatctaccgggcaatgaaactctcttggaggtgtctctggccatgtgtgtg	1275
QY	190	gcgttgagatgtcaacaagcagccgaatctgtgcggggcttcaagctcatcctgcac	249	DB	1210	ttcagttctcagggcgatctattgctctacacagatcgaaacagatgatagacggcaag	1269
DB	280	gcgctggagagcgtaagcgcaggaacatctctgcggactatgagctcaagctcac	339	DB	1276	tttgatgcagcggtctcggatggcagcttaccagcagcttcagacggttcaggcgc	1335
QY	250	agcaacagacgagatgagcccggtttggcgccagcgatgtacaaatctgtctctat	309	QY	1270	tacgaagaattgggttactacgatactcagttggataacctatctcgttggtaactgaa	1329
DB	340	caccacgacagaagtgtaccagggccaagccaccagtaactatatagctgctctac	399	DB	1336	tacaagaagattggctactatgacagcaccagagatgatcttctcgttgcacaaacagat	1395
QY	310	aataaacgcgaagactgatctgttggcaggatcagcagctgtgcacactgtagcc	369	QY	1330	caagtgttggtggcaaggttcctcaagatcgcaaatgtccaccatgttctcagcacc	1389
DB	400	aacgacctataagatcatcttctgtcgtgctcagctgtctcaccgctgtggtct	459	DB	1396	aaatggatggaggtgcccccagctgaccagacctggctatcaagacattccgcttc	1455
QY	370	gagctgcgaataatggaatctaatgtgtctctgtctacggggcctcgagtcggctctt	429	QY	1390	gtctcctgcattatttggatgtgcataatccagttggtgtgtgcataattcgttgc	1449
DB	460	gagctgtagagtggaactcattgtgttctctatgctccagctcaccagccctg	519	DB	1456	ctgtcaagaaccttcttctcctcgtctcagttctctccagcctgggcatgtcctagct	1515
QY	430	tcggtatgcgaacgattcccaactatttcgcaccccatccatcgcccgctgtgcacat	489	QY	1450	ttcgcttgatcatcttataatataatggaataagcagatagaagagtaatacacaatccctgc	1509
DB	520	tcaacccggcaggttcccaacttcttcgacgcacccatcagcaccactccacaac	579	DB	1516	gtgtctgtctgtcttataacatcacaactcacatgtccggttatataccagaactcac	1575
QY	490	ccaacgcgcatacagctgatgaagaaatcgctgctcgcgggtggtccattctgcagc	549	QY	1510	ccggttgcaatacagatcatgttatgttggtgtcatcatctgtctaaatctgtcatctta	1569
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QY	550	gcggaggaggtctttatcagaccgtagaggtatcgcgaatcgaatgcgaggtctgc	609	QY	1570	ctgggcatcgacgacgacttggcagcccgaggaatatccaaagatatgtcaagcgcg	1629
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QY	910	aacaatcagacaactatctacggaatgactgcagaggaatttcgacatcgactgaatcag	969	QY	1924	aactccatgt	1983
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Db 2293 tggcagtcggagcgacacacatgagacaggggtcatcgaccacaacaacagaggag 2352
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RESULT 10

AAZ06970
 ID AAZ06970 standard; cDNA; 2886 BP.

AC AC

AAZ06970;

15-NOV-1999 (first entry)

Human gamma-amino-butyric acid B receptor subunit GABABR1a cDNA.

KW Gamma-amino-butyric acid B receptor subunit; HG20; GABABR1a;
 depression; epilepsy; neuropsychiatric disorder; dementia;
 muscular contraction; central nervous system disorder; ss.

OS Homo sapiens.

Key Location/Qualifiers

1..2886

FT CDS

FT /*tag= a

FT /product= "GABABR1a"

FT /note= "gamma-amino-butyric acid B receptor subunit"

XX WO9940114-A1.

XX 12-AUG-1999.

XX 03-FEB-1999; 99WO-US02361.

XX 05-FEB-1998; 98US-0073767.

XX (MERI) MERCK & CO INC.

XX (MERI) MERCK FROSST CANADA INC.

XX (UYTE-) UNIV TEXAS HEALTH SCI CENT SAN ANTONI.

XX (USSH) US NAT INST OF HEALTH.

XX Bonner TI, Bonner TP, Clark J, Kolakowski LF, Liu Q;

XX McDonald T, Ng GYK;

XX WPI; 1999-527300/44.

XX P-PSDB; AAY29798.

XX New DNA encoding human and murine receptor subunits, useful for

XX identifying agonists and antagonists for treatment of depression,

XX epilepsy and neuropsychiatric disorders

XX Disclosure; Fig 18; 128pp; English.

XX The present sequence encodes a human gamma-amino-butyric acid (GABA)

XX B receptor (GABABR) subunit designated GABABR1a. The present invention

XX also describes the GABABR subunit designated HG20. Cells expressing

XX the new receptor subunits are useful for identifying GABABR agonists

XX and antagonists. HG20 proteins and their antagonists are useful for

XX inhibiting HG20 or GABABR function, useful for treating depression,

XX epilepsy, neuropsychiatric disorders, dementias, muscular contractions,

XX and central nervous system disorders.

XX Sequence 2886 BP; 632 A; 822 C; 797 G; 635 T; 0 other;

SQ

Query Match

Best Local Similarity 22.6%; Score 569.4; DB 20; Length 2886;

54.8%; Pred. No. 4.3e-170;

Matches 1231; Conservative 0; Mismatches 981; Indels 33; Gaps 4;
 QY 130 ccgataccggrcaaaagagagatggcagggggccaggcggtatgctgtccacaagaactg 189
 Db 523 ctgtttcccatgagcgggggctggccaggggccaggcctgccagccgcggtggagatg 582
 QY 190 gcgttgatgatgtcaacaagcagccgaatctgctgcgggcttcaagctcatctgcac 249
 Db 583 gcgctggaggacgtgaatagccgaggacatcctgcggactatgactgaactcaatc 642
 QY 250 agcaacgacagcagtgtagcccggtttggcgccagcggtgagtacaactctctctat 309
 Db 643 caccacgacagcaagtgtgatccaggccaagccaagtaacctatatgaactctctac 702
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 QY 370 gaggctgccaaaatgtgaaatctaattgtctgtctgtacaggggctcgagtcggctctt 429
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 Db 1459 ggaaggcgccgttctgtgtgcctggaggacttcaactacaacaaccagaccattacc 1518
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    || || || || || || || || || || || || || || || || || || || || || ||
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RESULT 11
AAX58054
ID AAX58054 standard; cDNA to mRNA; 2886 BP.
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AC AAX58054;
XX
DT 21-JUL-1999 (first entry)
XX
Human GABAB receptor la coding sequence.
XX
GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;
transient lower oesophageal sphincter relaxation; spasticity; emesis;
gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;
irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;
autoimmune disease; neoplastic disease; infectious disease; therapy; ss.
XX
Homo sapiens.
XX
PN WO9921890-A1.
XX
PD 06-MAY-1999.
XX
PF 27-OCT-1998; 98WO-SB01947.
XX
PR 17-JUL-1998; 98SE-0002575.
PR 27-OCT-1997; 97SE-0003914.
PR 16-MAR-1998; 98SE-0000864.
XX
(ASTR ) ASTRA AB.
XX
Ekstrand J;
XX
WPI; 1999-302985/25.
P-PSDB; AAX14101.
XX
Polynucleotides encoding human and canine gamma aminobutyric acid
type B receptors, used to screen for compounds that are inhibitors
of transient lower oesophageal sphincter relaxations
XX
Claim 4; Page 79-84; 222pp; English.
XX
This sequence encodes a human gamma aminobutyric acid type B (GABAB)
receptor of the invention. Nucleic acid molecules encoding GABAB
receptors can be used to screen for compounds that are inhibitors of
transient lower oesophageal sphincter relaxations (TLESR). They can also
be used to screen for agonists or antagonists of the GABAB receptors.
Inhibitors of TLESR are useful for treating gastro-oesophageal reflux
disease. Other uses of GABAB receptors, such as human GABAB Ric or 1d,
comprise diagnosis or treatment of conditions related to GABAB
dysfunction, e.g. epilepsy, psychiatric disorders, emesis, irritable
bowel syndrome, dyspepsia, spasticity, arthritis, allergies, autoimmune
diseases, neoplastic diseases, pain and infectious disease.
XX
Sequence 2886 BP; 632 A; 821 C; 798 G; 635 T; 0 other;
SQ
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Query Match 22.6%; Score 569.4; DB 20; Length 2886;
Best Local Similarity 54.8%; Pred. No. 4.3e-170;
Matches 1231; Conservative 0; Mismatches 981; Indels 33; Gaps 4;

QY 130 ccgatagcggccaagagagatggcagggcgccagcgtgatcctgccacaagactg 189
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Db 523 ctgtttcccatgagcgggggtggtgccagggggccagcctgccagcccggtgagatg 582
|| || || || || || || || || || || || || || || || || || || || || ||


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1348 aaatggattgagggtcccccagctgaccagaccctggcctacaaagacattccgcttc 1407
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1408 ctgtcacagaactcttattctcgtctcagttctctccagctggtggaattgtcttagct 1467
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2365 gaggagcgtgtctcgaactgcgcc 2389
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RESULT 13

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AA293411
ID AA293411 standard; cDNA; 2914 BP.
XX
AC AA293411;
XX
DT 24-JUL-2000 (first entry)
XX
DE Human GABAB1A receptor coding sequence.
XX
KW GABAB1A receptor; G-protein; disease; treatment; detection;
KW therapy; antibody; immune response; infection; cancer; diabetes;
KW obesity; anorexia; bulimia; Parkinson's disease; heart failure;
KW hypertension; hypertension; urinary retention; osteoporosis;
KW angina pectoris; myocardial infarction; stroke; ulcers; asthma;
KW allergy; benign prostatic hypertrophy; migraine;
KW neurological disorders including anxiety; schizophrenia;
KW depression; dementia; Huntington's disease;
KW Gilles de la Tourette's syndrome; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..2883
FT /*tag= a
FT /product= GABAB1A receptor
XX
PN WO200012106-A1.
XX
PD 09-MAR-2000.
XX
PF 30-AUG-1999; 99WO-US19435.
XX
PR 01-SEP-1998; 98US-0144779.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI Elshourbagy NA;
XX
DR WPI; 2000-237771/20.
DR P-PSDB; AAY83145.
XX
PT New GABAB1A polypeptide useful for diagnosis, treatment and prevention
PT of diseases associated with its expression including infections,
XX psychotic and neurological disorders and cancer
PS Claim 2; Page 33-34; 38pp; English.
XX
CC The GABAB1A receptor is believed to be a member of the GABAB
CC family of polypeptides. They are therefore of interest because
CC members of the purinergic 7TM receptor family (G-protein coupled
CC receptors) of genes are involved in a number of biological and
CC disease manifestations. They are also a successful target for
CC pharmaceutical intervention. Antibodies directed against GABAB1A
CC and its peptides can be used to treat bacterial, fungal, protozoan
CC and viral infections, pain, cancers, diabetes, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC myocardial infarction, stroke, ulcers, asthma, allergies, benign
CC prostatic hypertrophy, migraine, vomiting, psychotic and
CC neurological disorders including anxiety, schizophrenia, depression,
CC dementia and severe mental retardation and dyskinesias such as
CC Huntington's disease or Gilles de la Tourette's syndrome. The
CC GABAB1A polypeptide or a vector comprising a sequence encoding the
CC polypeptide can be used to induce an immunological response in a
CC mammal to protect against disease. The presence or absence of a
CC mutation in the nucleotide sequence encoding the GABAB1A polypeptide
CC can be detected in the genome of a subject and/or the presence or
CC amount of expression of the polypeptide in a sample from the subject
CC can be analysed and used to diagnose a disease or susceptibility to a
CC disease related to the expression or activity of GABAB1A.
CC Diagnosis can be measured at the RNA level using nucleic acid
CC amplification, e.g. polymerase chain reaction, RNase protection or
CC Northern blotting or at the protein level by radioimmunoassay,
```

CC competitive-binding assays, Western blot analysis or ELISA assays
CC (enzyme linked immunosorbent assay).

XX Sequence 2914 BP; 638 A; 825 C; 816 G; 635 T; 0 other;

Query Match 22.6%; Score 569.4; DB 21; Length 2914;
Best Local Similarity 54.8%; Pred. No. 4.3e-170;
Matches 1231; Conservative 0; Mismatches 98; Indels 33; Gaps 4;

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```

```
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DB 1876 cccaacctgaacaacctgactgctgtggtgctcactggctttagctgtgtctctccc 1935
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DB 2293 atgaatacatggttggcatcttctatggttacaagggtggtgctgctgctggtgggaac 2352
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QY 2104 attgcatcgaacagacgcgctccttggcttggcttggcttagctgtgattattgtgtg 2163
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DB 2473 ctgtccagcagcagatgagccttggccttggcctctctctgcatagttttctctcc 2532
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Qy	2224	gataaggcggaatcgaaatacaatcccgtattcagccatctcgaaagagcgaagaacgc	2283
Db	2593	tggcagtcgagcgagcgacaccatgaagacaggtgatcgaccaccaacaacacgaggag	2652
Qy	2284	tatcagaaactgttaccgaaacagcgaatgcaacgatttaataacacagaagaggaa	2343
Db	2653	gagaagtcgccgctgttgagaagaggaaccgtgaactggaaaagatcattgtgtgagaaa	2712
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Db	2713	gaggagcgtgctcgaactgcgc	2737
RESULT 14			
ID	AAV10267		
ID	AAV10267	standard; cDNA to mRNA; 2924 BP.	
AC	AAV10267;		
DT	03-JUN-1998	(first entry)	
DE	Human GABA-BR1b receptor cDNA.		
XX	Gamma-aminobutyric acid; GABA-BR1a/b receptor; human; brain; agonist;		
KW	inhibitory neurotransmitter; peripheral nervous system; antagonist;		
KW	treatment; dementia; depression; anxiety; bronchial inflammation; asthma;		
KW	epilepsy; cognitive function; ds.		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
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FT		/*tag= a	
FT		/product= GABA-BR1b	
XX	W09746675-A1.		
XX	11-DEC-1997.		
XX	19-MAR-1997;	97WO-EP01370.	
XX	22-NOV-1996;	96US-0756091.	
PR	30-MAY-1996;	96US-0655716.	
XX	(NOVS) NOVARTIS AG.		
XX	Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;		
XX	WPI; 1998-042183/04.		
DR	P-PSDB; AAW40119.		
XX	Purified GABA-B receptor or receptor protein - and antagonists of		
PT	these which may be useful in treating nervous system disorders		
XX	Claim 3; Page 79-86; 108pp; English.		
XX	This cDNA sequence encodes a novel human GABA-B receptor protein,		
CC	GABA-BR1b. GABA (gamma-aminobutyric acid) is the major inhibitory		
CC	neurotransmitter found in the brain and peripheral nervous system		
CC	and this receptor may be used for the identification of GABA-B		
CC	receptor agonists and antagonists. Such proteins may be used in		
CC	treatment of dementia, depression, anxiety, epilepsy, spasticity,		
CC	bronchial inflammation or asthma or to improve cognitive function.		
CC	GABA-B receptor ligands and probes derived from this sequence can be		
CC	used to assay for GABA-B receptors or DNA encoding them.		
XX	Sequence 2924 BP; 628 A; 852 C; 793 G; 651 T; 0 other;		
SQ			

Query Match				22.6%	Score 569.4;	DB 19;	Length 2924;
Best Local Similarity				54.8%;	Pred. No. 4.3e-170;		
Matches 1231;				Conservative	0;	Mismatches 981;	Indels 33; Gaps
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QY	190	gggttgatgatgtc	aaacagcagcggaattcgtctgcgggcttcaagctcatctcgtcac	249			
DB	400	ggcctgaggagcgt	gaatagccgagggacatctctgcggactatgagctcaagctcatc	459			
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DB	460	caccacgacgca	agtgtgtccaggccagccaccaagtaacctatagctgctctac	519			
QY	310	aataaacgcgca	aaagctgatgtgttgccaggatgcagcagcggtctgcacacactgtagcc	369			
DB	520	aacgaacctatca	agatcatctctatgcttggctgagctctgtctccagctggtggct	579			
QY	370	gaggctgc	caaaattggaattgtctctgtacaggggctcgagtcgggctctt	429			
DB	580	ggggctgt	aggatgggaaccttattgtctttctatggctccagctcaaccgacctg	639			
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DB	640	tcaaacggcag	cggtttccccactttcttcgaacgcaccatcagccacactccaac	699			
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DB	700	cttaccgcggt	gaacctcttgtaaaagtgggctgggaagaagattgtaccatccagcag	759			
QY	550	gcggaggaggt	ctttatatcgacgctagagatctcgagaatcgatgcattggaggtggc	609			
DB	760	accactgaggt	cttctactctgcactctggagcacttggaagacgagtgaaggaggtcgga	819			
QY	610	gttgaatcg	tgaactagacaaatctttctatccgatccacagacgcgtgcgaatttg	669			
DB	820	attgagatt	actttccgccaagtattctctcagatccagctgtgcccgtcaaaaacctg	879			
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DB	880	aagcgcaggat	gccgaatcatctgtgggactttctatgagactgaagccgcggaaaagt	939			
QY	730	ctctcgaaat	gtacaaaacgacgactatagccgagctcatgtgtggttttatggc	789			
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DB	1000	tgttatgtc	gacaatttggt-----tcaagatctacgaccttctatcaactgcacagt	1053			
QY	850	gaacagatc	gaaatagctgcgcgaaggacatctgacaacggaagcgctcatgttggaaatcag	909			
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QY	910	aaacatcga	caacaactatctcgaatgactgcagaggaatttcgacatcgactgaatcag	969			
DB	1114	gcaatacc	ccgcagcaatttccaacatgacatccacggaaattgttgggagaacataccaag	1173			
QY	970	gcgctaact	cgagggtttacgacattaaaccaagatcgctatccggagggatatacaggag	1029			
DB	1174	cgatgaaa	agacacacctgaggaga-----caggaggcttccaggag	1215			
QY	1030	gcgcgaact	cgctacagatgcagtgtaggagtgtggcttttgcatttcaacagaccatggaa	1089			
DB	1216	gcaccgtgc	ctatgatgcatactggccttggcactgggccccctggaacagacatctgga	1275			
QY	1090	cgatigaca	caaccgggaagaaatctctgagggtatttacctatatacgcgcaaggagatgcc	1149			
DB	1276	gagagc	gcggttctgtgtgcgcttggaaggacttcaactacaaacaccagaccattacc	1335			
QY	1150	gatgaatat	ctacgtgccatgaaactccacaactttctgggtgtatcggtgtgtgtgtggca	1209			

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Db 1336 gaccaaatctacggggaagaatctcttcgtcccttggaggtgtctctggtccatctggtg 1395
QY 1210 ttcaagttctcagggcgatctgtatgtctcttacacagatcgacaagatgatagacggcgaag 1269
Db 1396 ttgatccagcggctctcggatggcagcgcttctacgacgcttcagggtgcgcagc 1455
QY 1270 taagagaagttgggttactacgatactcagttggtgataacacctatcctcgttgtaataactaa 1329
Db 1456 tacaagaagattggtctactatgacagaccacaagatgatcttctcgtgtccaaaacagat 1515
QY 1330 cagtggattggtggcgaaggttccccaagatcgcaaatgtccaccatgttccatcagcacc 1389
Db 1516 aaatggattggaggggtccccccagcgtgaccagaccctggctacaaagacatcccgcttc 1575
QY 1390 gttccttgccattattgtgtgcatgtgcacaatatccagttgtggcatattcgtttgcc 1449
Db 1576 ctgtcacagaaactcttatctcgtctcagttctctccagccgtggcattgtcctagct 1635
QY 1450 ttgccttgatcatctttaatatatgaaataagaatagaagagtaatacaatccctcgcat 1509
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QY 1690 cgtgtgcatcgttttacaaaa-----aagcaaaactgaccacaaagaaaagtggaa 1743
Db 1876 tgggtccacacggtcttcacaaaagaagaagaaggaggtggaggaactctggaa 1935
QY 1744 ccttggagctatacacatggtttcgggcttattatacaatagatttagtgatatctact 1803
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QY 1804 tcattgagatcttttgatccgctcagcgtttatctcgaatactcccaactcgaatccca 1863
Db 1996 atctggcagatcgtggaccctctgcacggaccattgagacatttgccaagggagaaact 2055
QY 1864 gtatctactatgatattataaataacgtccagagcttgagcattgtgaaagtcaacgc 1923
Db 2056 aaggaagatatgtacg---tctctattctgccacgctggagcattgcagctccaggag 2112
QY 1924 aactccatgtgtgtgtgtgtatcacgcttcgaagggtcaatccctggtgttttgccctc 1983
Db 2113 atgaatacatggtctgcatctttctatggttcaaaagggctgctgctcgtcgtggaaatc 2172
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Db 2173 ttctgtctatgagaccaagagtggtcccaactgagaagatcaatgatcacccgggctgtg 2232
QY 2044 ggcagagcatctataacgtgtgtgtcgttcttgcctgtataacagctccgggtggcagtgctc 2103
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QY 2164 ttctgaagcatgctgctgatatatttgcccaaggtcattgagttatcgtcatccccaag 2223
Db 2353 tatataactctgtgtgtcttctgtgtcccaagatgcgcagcgtgatcaccccgaggga 2412
QY 2224 gataagcccgaaatcgaataatcccgattccagccatctatcgaagagagacgaagacgc 2283

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Db 2413 tggcagctcgagggcgaggacaccatgaagacaggggtcatcgaccacacacagagag 2472
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Db 2473 gagaagtcctcggtgtgttgagaagagaacctggaactgaaaagatcattgctgagaaa 2532
QY 2344 aagattcagagtcctcgacagcgtc 2368
Db 2533 gaggagcgtgtctctgaactgcgc 2557

RESULT 15
AAX90920
ID AAX90920 standard; DNA; 3464 BP.
XX
AC AAX90920;
XX
DT 17-JAN-2000 (first entry)
XX
DE Human GABABR1a receptor subtype DNA.
XX
KW GABABR1a receptor protein; cloning; rat brain; GABABR2; GABAB receptor;
human gamma-aminobutyric acid receptor; metabotropic receptor; screening;
synaptic transmission; GABABR1b; cloned receptor; splice variant;
modulatory agent; molecular activity assay; antispastic; anti-addictive;
antineurodegeneration; analgesic; cardiovascular activity; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS l..2886
FT FT /*tag= a
FT FT /product= "Human GABABR1a receptor protein"
XX
PN WO951636-A2.
XX
PD 14-OCT-1999.
XX
PF 02-APR-1999; 99WO-US07352.
XX
PR 03-APR-1998; 98US-0080676.
XX
PA (NPSP-) NPS PHARM INC.
XX
PI Garrett JE, Simin RT, Busby JG, Stormann TM;
XX
WPI: 1999-610994/52.
XX
P-PSDB; AAX90920.
XX
PT Novel nucleic acids, used to screen for specific modulators, e.g. for
treating spasticity or Alzheimer's disease
XX
PS Disclosure; Fig 1A-1N; 78pp; English.
XX
CC The present sequence encodes GABABR1a receptor protein cloned from rat
brain. This is closely related to GABABR2. GABAB receptors are
metabotropic receptors that modulate synaptic transmission in brain.
GABABR1a differs from GABABR1b in that the N-terminal 147 residues are
replaced by 18 amino acids. Both of these cloned receptors appear to be
splice variants. They are expressed in cells that express GABABR2. This
nucleotide sequence is used to screen for specific modulators. These
modulators have antispastic, antineurodegeneration, analgesic, anti
-addictive, cardiovascular activities.
XX
SQ Sequence 3464 BP; 736 A; 998 C; 926 G; 802 T; 2 other;

Query Match 22.6%; -Score 569.4; DB 20; Length 3464;
Best Local Similarity 54.8%; Pred. No. 4.9e-170;
Matches 1231; Conservative 0; Mismatches 981; Indels 33; Gaps 4;
QY 130 ccgatagcggcgaagaggagatggcagggcgccagcggtgtatgctgcacaaagactg 189

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Db 523 ctgtttcccatgagcgggggctggccagggggccaaggcctgccagcccgcggtggagatg 582
QY 190 gcgttgatgatgcaacaagcagccgaatctgtgctgcgggcttcaagctcatctcgtcac 249
Db 583 gcgtggagagctggaatgacgcagggacatctctgcggactatgactcaagctcatc 642
QY 250 agcaacgacagcagtgtagcccggtttggcgccagcgtgatatacaatctctctat 309
Db 643 caccacgacgcaagtgtgataccgggccaagcccaagtagtaacctatagagtgctctac 702
QY 310 aataaacccgaaaagctgatgtgtgacagatgacagcagcagcgtctgcaccactagcc 369
Db 703 aacgacctatcaagatcatctctatgctgtgcagctctgtctccacgctgtggt 762
QY 370 gaggctgccaaaaagtgaatctaatgtgtctgtctacggtgcgtcagtcgcggtctt 429
Db 763 gaggctgtaggtggaacctatgtgttctctatggtctccagctcaccagccctg 822
QY 430 tcggatcgcaaacgattccccactctattccgacccatccatcgccacggtgcacaat 489
Db 823 tcaaacggcagcgtttccccactttctccgaagcagcccatcagccacactccacaac 882
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QY 850 gaacagatcggaatagctgcgaaggacatctgacaacgggaagcgtcatgtggaatcag 909
Db 1237 gatgagatgactgaggcgtgaggggccacatccacatcagatgagattgtctgctgaact 1296
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Db 1459 ggaaggcgcgttctgtgtgctgggaggttcaactcaacaacagacctacc 1518
QY 1150 gatgaattacgctgcctgaactccacaataatttctgggtgtgtatcggtgtgtggca 1209
Db 1519 gaccaaatctaccgggcaatgaactcttctgttgggggtgtctctggtccatgtgtg 1578
QY 1210 ttcatctcagggcgatcgtattgtctcttacacagatcgaaacagatgatagacggcag 1269
Db 1579 ttgtatgcagcggctctcgtgtagtggaatggaacgtttatcgagcagcttcaagggtggcagc 1638

QY 1270 tacgagaagttgggtttactacgatactcagttggataacctatctcgtgttgaatactgaa 1329
Db 1639 tacaagaagattggctactatgacgaccagaagatgatcttctcgtgttccaaacagat 1698
QY 1330 cagtggattggtggcaaggttctcaagatcgcaaatgttcacccatgttctcagcacc 1389
Db 1699 aatggattggagggtcccccagctgaccagacctggttcatcaagacattccgcttc 1758
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Db 1759 ctgtcacagaaactctttatctcgtctcagttctctccagctggcgattgtcctagct 1818
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Db 2656 gagaagctccggtgtgtggagaaggagaccgtgaactggaaaagatcattgtctgagaaa 2715

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2002, 01:40:55 ; Search time 3542.84 Seconds
(without alignments)
11748.310 Million cell updates/sec

Title: US-09-715-962-1

Perfect score: 2523

Sequence: 1 atgcgaagatgacaag.....caatcacacaagtgtgtag 2523

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:**

1: gb_ba:**
2: gb_htg:**
3: gb_in:**
4: gb_om:**
5: gb_ov:**
6: gb_pat:**
7: gb_ph:**
8: gb_pl:**
9: gb_pr:**
10: gb_ro:**
11: gb_sts:**
12: gb_sy:**
13: gb_un:**
14: gb_vi:**
15: em_ba:**
16: em_fun:**
17: em_hum:**
18: em_in:**
19: em_om:**
20: em_or:**
21: em_ov:**
22: em_pat:**
23: em_ph:**
24: em_pl:**
25: em_ro:**
26: em_sts:**
27: em_sy:**
28: em_un:**
29: em_vi:**
30: em_htgo_hum:**
31: em_htgo_inv:**
32: em_htgo_rod:**
33: em_htg_hum:**
34: em_htg_inv:**
35: em_htg_rod:**
36: em_htg_other:**

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query Match	Length	DB	ID	Description
1	2523	100.0	2523	3	AF318272	AF318272 Drosophil
2	672	26.6	53444	2	AC019747	AC019747 Drosophil
3	672	26.6	184682	3	AC092238	AC092238 Drosophil
4	672	26.6	266308	3	AE003646	AE003646 Drosophil
5	672	26.6	303043	3	DROSADH05	AE003411 Drosophil
6	570.6	22.6	2886	6	AX054691	AX054691 Sequence
7	569.4	22.6	2535	9	HSA012186	AJ012186 Homo sapi
8	569.4	22.6	2700	9	HSA012187	AJ012187 Homo sapi
9	569.4	22.6	2886	9	HSA012185	AJ012185 Homo sapi
10	569.4	22.6	2928	9	HSB225029	AJ225029 Homo sapi
11	569.4	22.6	3192	9	AF099148	AF099148 Homo sapi
12	569.4	22.6	4281	9	HSB012288	AJ012288 Homo sapi
13	569.4	22.6	4445	9	HSB225028	AJ225028 Homo sapi
14	566.8	22.5	4220	9	HSBTHL1	Y11044 Homo sapien
15	564.4	22.4	2535	10	AF120255	AF120255 Mus muscu
16	564.4	22.4	3118	10	AF008649	AF008649 Mus muscu
17	563.6	22.3	4220	6	AX054692	AX054692 Sequence
18	558	22.1	2883	6	AX054688	AX054688 Sequence
19	558	22.1	4365	10	AF114168	AF114168 Mus muscu
20	554.8	22.0	2535	10	RNCABAB1B	Y10370 R.norvegicu
21	554.8	22.0	2883	10	RNCABAB1A	Y10369 R.norvegicu
22	549.2	21.8	3202	10	AB016161	AB016161 Rattus no
23	460.8	18.3	3000	10	AB016160	AB016160 Rattus no
24	460.8	18.3	4380	10	AF283276	AF283276 Rattus no
25	377.6	15.0	1740	9	AF301005	AF301005 Homo sapi
26	222.4	8.8	5459	10	AF058795	AF058795 Rattus no
27	220.2	8.7	2823	10	AF074482	AF074482 Rattus no
28	219.2	8.7	3288	6	AX023740	AX023740 Sequence
29	219.2	8.7	3288	10	AF109405	AF109405 Rattus no
30	219.2	8.7	5614	10	RNO011318	AJ011318 Rattus no
31	211.6	8.4	3155	9	AF099033	AF099033 Homo sapi
32	211.6	8.4	3240	9	AF095784	AF095784 Homo sapi
33	210	8.3	2826	6	AX023742	AX023742 Sequence
34	210	8.3	2826	9	AF074483	AF074483 Homo sapi
35	210	8.3	3075	9	AF069755	AF069755 Homo sapi
36	210	8.3	3480	6	AX054669	AX054669 Sequence
37	210	8.3	5786	9	AF056085	AF056085 Homo sapi
38	208.4	8.3	2826	9	HSB012188	AJ012188 Homo sapi
39	175.8	7.0	3663	3	AF318273	AF318273 Drosophil
40	175.8	7.0	3989	3	AF145639	AF145639 Drosophil
41	162.2	6.4	2887	6	E37093	E37093 GABA BP pol
42	132.8	5.3	1318	6	E37094	E37094 GABA BP pol
43	92.8	3.7	10147	10	RNCABA1S1	AF110796 Rattus no
44	92.8	3.7	47026	3	CBRG41B17	AC084584 Caenorhab
45	87	3.4	3918	3	AF318274	AF318274 Drosophil

ALIGNMENTS

RESULT	1	AF318272	2523 bp	mrna	INV	28-FEB-2001
LOCUS		Drosophila melanogaster metabotropic GABA-B receptor subtype 1				
DEFINITION		(GABA-B-R1) mRNA, complete cds.				
ACCESSION		AF318272				
VERSION		AF318272.1	GI:13160941			
KEYWORDS		fruit fly.				
SOURCE		Drosophila melanogaster				
ORGANISM		Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
REFERENCE		1 (bases 1 to 2523)				
AUTHORS		Mezler.M., Muller.T. and Raming,K.				
TITLE		Cloning and functional expression of GABA-B receptors from Drosophila				
JOURNAL		Eur. J. Neurosci. 13 (3), 477-486 (2001)				
PUBMED		11168554				
REFERENCE		2 (bases 1 to 2523)				

Db	1561	GTCACTTACTGGGCATCGACGGAGCGCTTTGTGAGCCCGGAGGAATATCCAAAGATATGT	1620
QY	1621	caagcgggcttggttaactatccacgggttttacactagatacaggtgctatgttcagc	1680
Db	1621	CAAGCGGGCTTGGTTACTATCCACCGGTTTACACTAGATACGGTGTATGTTTCAGC	1680
QY	1681	aaggtctgcgctgcatcgctttacacaaagcaaaaactgaccccaagaaaaaagt	1740
Db	1681	AAGGTCTGGCGTGTGCATCGTTTACAAACAAAGCAAAAACCTGACCCAAAGAAAAGTG	1740
QY	1741	gaaccttgaagctatcacaccatggttttcggggtctattatcaatagatttagtgatatta	1800
Db	1741	GAACCTTGAAGCTATACACCATGTTTCGGGCTATTATCAATAGATTTAGTGATATA	1800
QY	1801	ctctatggcagatctttgatccgctcagcggttatctcgaacattccccactogaagat	1860
Db	1801	CTCTATGGCAGATCTTTGATCCGCTCAGCGTTATCTCGAAACATTTCCCACTCGAAGAT	1860
QY	1861	caagtatctactgatgatattataaatacgtccagagcttgacgattgtgaaagtcaa	1920
Db	1861	CCAGTATCTACTACTGATGATATTAATAATACGTCAGAGCTTGAGCATTTGTCAAAGTCAA	1920
QY	1921	cgaactccatgtggttgggtcttgatacggcttcaagggttaactcctggtgtttggc	1980
Db	1921	CGCAACTCCATGTGTTGGGTCTTGATACGGCTTCAAGGGGCTAATCTCGTGTTCGC	1980
QY	1981	ctcttttggcgtacgagacgcgtccattaaagtgaacagatcaacgattcgcgttat	2040
Db	1981	CTCTTTTGGCGTACGAGACGCGCTCCATTAAAGTGAAACAGATCAACGATTCGCGTTAT	2040
QY	2041	gtgggcatgagatctataacgctggtcgtctcttgctgataacagctcccggtggcgatg	2100
Db	2041	GTGGGATGAGCATCTATAACGTGGTGTCTCTTTGCCCTGATTAACAGCTTCCCGTGGCGATG	2100
QY	2101	gtcatgtcatcgcaacaggcgcgtcttgccttgccttgcctgctagctgtgatattctgt	2160
Db	2101	GTCAATGTCATCGCAACAGGACGCGCTCTTTGCCCTTGGTTCCTAGCTGTGATATCTGT	2160
QY	2161	tgttctcaagcatgctgtgatattgtgccaaggctcattgaggttatcgtcatccc	2220
Db	2161	TGTTTCTTAAGCATGCTGCTGATATTTGTGCCAAAGGTTCATTGAGGTTTATACGTCATCCC	2220
QY	2221	aagdataagccgaatcgaatacaaatcccgattcagccatatacgaagagagcagaagaa	2280
Db	2221	AAGGATAAGCCGAATCGAAATACAATCCGATTACGCCATATCGAAAGAGAGCGAAGAA	2280
QY	2281	cgtatcagaacttgttaccgaaacagcaattgcaacgattataaacaacagaagag	2340
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LOCUS	53444 bp	DNA	HTG
DEFINITION	Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***		03-JAN-2000
ACCESSION	AC019747		

VERSION	AC019747.1	GI:6665150
KEYWORDS	HTG: HTGS_PHASE2.	
SOURCE	fruit fly.	
ORGANISM	Drosophila melanogaster	
REFERENCE	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	
AUTHORS	1 (bases 1 to 53444)	
TITLE	Adams, M. and Venter, J.C.	
JOURNAL	Direct Submission	
COMMENT	Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA This sequence was identified as CDM:10210817 by the submitter. * NOTE: This is a 'working draft' sequence. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved.	
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DEFINITION	Drosophila melanogaster, chromosome 2L, region 36X-36X, BAC clone BACR03D18, complete sequence.
ACCSSION	AC092238
VERSION	AC092238.1 GI:14578119
KEYWORDS	HTG.
SOURCE	fruit fly.
ORGANISM	Drosophila melanogaster
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 184682)
REFERENCE	Celniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,
AUTHORS	

Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskaas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.

Sequencing of *Drosophila* chromosome 2L, region 36X-36X

Unpublished

2 (bases 1 to 184682)

Celniker, S.E., Adams, M.D., Krommiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskaas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.

This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive web site (<http://www.fruitfly.org/sequence/>) or send email to bdqap@fruitfly.berkeley.edu.

FEATURES
source

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Location/Qualifiers
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LOCUS Drosophila melanogaster genomic scaffold 14200001386055 section 39
DEFINITION of 63, complete sequence.
ACCESSION AE003646 AE002690
VERSION AE003646.2 GI:10728794
KEYWORDS HTG.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 266308)

Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D.,

Amann,T.D., Baxendale,J., Bayraktaroglu,L., Beasley,E.M., Beeson,K.Y.,

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Brandon,R.C., Rogers,Y.H., Blazer,V.G., Champ,M., Pfeiffer,B.D.,

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Stapleton,M., Skupski,M.P., Smith,T., Spier,E., Spradling,A.C.,

Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wasserman,D.A.,

Weinstock,G.M., Weissbach,J., Williams,S.M., Woodage,T.,

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Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H.,

Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O.,

Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.

The genome sequence of Drosophila melanogaster

Science 287 (5461), 2185-2195 (2000)

20196006

2 (bases 1 to 266308)

REFERENCE

AUTHORS Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.

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TITLE      Direct Submission
JOURNAL    Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
            Rockville, MD, USA
COMMENT    On Oct 9, 2000 this sequence version replaced gi:7298191.
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SOURCE	fruit fly.		
ORGANISM	Drosophila melanogaster		
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AUTHORS	1 (bases 1 to 303043)		
REFERENCE	Ashburner,M., Misra,S., Rote,J., Lewis,S.E., Blazej,R., Davis,T., Doyle,C., Galle,R., George,R., Harris,N., Hartzell,G., Harvey,D., Hong,L., Houston,K., Hoskins,R., Johnson,G., Martin,C., Moshrefi,A., Palazolo,M., Reese,M.G., Spradling,A., Tsang,G., Wan,K., Whitelaw,K., Celniker,S. and Rubin,G.M.		
TITLE	An exploration of the sequence of a 2.9-Mb region of the genome of Drosophila melanogaster: the Adh region		
JOURNAL	Genetics 153 (1), 179-219 (1999)		
MEDLINE	99403001		

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DEFINITION ACCESSION AJ012186
VERSION AJ012186.1 GI:3776093
KEYWORDS GABAB receptor; gabab-R1 gene; subunit 1b.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2535)
AUTHORS White,J.H., Wise,A., Main,M.J., Green,A., Fraser,N.J., Disney,G.H.,
Barnes,A.A., Enson,P., Foord,S.M. and Marshall,F.H.
TITLE Heterodimerization is required for the formation of a functional
GABA(B) receptor
JOURNAL Nature 396 (6712), 679-682 (1998)
MEDLINE 99087321
REFERENCE 2 (bases 1 to 2535)
AUTHORS Fraser,N.J.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-1998) Fraser N.J., Receptor Systems, Cellular
Sciences, Glaxowellcome, Medicines Research Centre, Gunnels Wood
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REFERENCE 1 (bases 1 to 2700)
AUTHORS Fraser,N.J.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-1998) Fraser N.J., Receptor Systems, Cellular
Sciences, GlaxoWellcome, Medicines Research Centre, Gunnels Wood
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GABA-B receptor.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 2928)

AUTHORS

Kaupmann,K.

TITLE

Direct Submission

JOURNAL

Submitted (12-MAR-1998) Kaupmann K., TA Nervous System, Novartis
Pharma AG, K-125.6.20, CH-4002 Basel, SWITZERLAND
2 (bases 1 to 2928)
Kaupmann,K., Schuler,V., Mosbacher,J., Bischoff,S., Bittiger,H.,
Heid,J., Froestl,W., Leonhard,S., Pfaff,T., Karschin,A. and
Bettler,B.
Human gamma-aminobutyric acid type B receptors are differentially
expressed and regulate inwardly rectifying K⁺ channels
Proc. Natl. Acad. Sci. U.S.A. 95 (25), 14991-14996 (1998)

MEDLINE

99061981

FEATURES

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RESULT 13

HSA225028

LOCUS HSA225028 4445 bp mRNA

PRI 11-DEC-1998

DEFINITION Homo sapiens mRNA for GABA-B 1a receptor.

ACCESSION AJ225028

VERSION AJ225028.1 GI:3892593

KEYWORDS GABA-B receptor.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


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RESULT 14
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LOCUS Homo sapiens mRNA for GABA-BR1a (hGBl1) receptor.
DEFINITION Y11044
ACCESSION Y11044
VERSION Y11044.1 GI:2826760
KEYWORDS GABA-B receptor.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE

1 (bases 1 to 4220)

AUTHORS

Grifa,A., Totaro,A., Rommens,J.M., Carella,M., Roetto,A., Borgato,L., Zelante,L. and Gasparini,P.

TITLE

GABA (gamma-amino-butyric acid) neurotransmission: identification and fine mapping of the human GABAB receptor gene

JOURNAL

Biochem. Biophys. Res. Commun. 250 (2), 240-245 (1998)

MEDLINE

98440782

REFERENCE

2 (bases 1 to 4220)

AUTHORS

Gasparini,P.

TITLE

Direct Submission

JOURNAL

Submitted (04-FEB-1997) P. Gasparini, Servizio de Genetica Medica - IRCS, 'Ospedale CSS', Via Cappuccini, 71013 S Giovanni, Rotondo (FG), ITALY

REMARK

revised by submitter 28-JAN-98

COMMENT

On Jan 31, 1998 this sequence version replaced gi:2370108.

FEATURES

Location/Qualifiers

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BASE COUNT

ORIGIN

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Best Local Similarity

54.7%; Pred. No. 1.3e-155;

Matches 1229; Conservative

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QY 250

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BASE COUNT      578 a 718 c 666 g 573 t
ORIGIN

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Best Local Similarity 54.9%; Pred. No. 6e-155;
Matches 1242; Conservative 0; Mismatches 981; Indels 39; Gaps 5;

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:12:33 ; Search time 32.13 Seconds
(without alignments)
3824.113 Million cell updates/sec

Title: US-09-715-962-2
Perfect score: 4374
Sequence: 1 MRKDMTSDGATFWIFLLCL.....LINSAAHATPAATLAITGGE 840

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SP TREMBL.17.*
- 2: SP Archaea.*
- 3: SP Bacteria.*
- 4: SP Fungi.*
- 5: SP Human.*
- 6: SP Mammal.*
- 7: SP MHC.*
- 8: SP Organelle.*
- 9: SP Phase.*
- 10: SP Plant.*
- 11: SP Rodent.*
- 12: SP Virus.*
- 13: SP Vertebrate.*
- 14: SP Unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4374	100.0	840	5 Q9BML7	Q9bml7 drosophila
2	3317	75.8	1713	5 Q9V3Q9	Q9v3q9 drosophila
3	1746.5	39.9	816	5 Q9N502	Q9n502 caenorhabdi
4	1186.5	27.1	1220	5 Q9BML6	Q9bml6 drosophila
5	1183.5	27.1	1221	5 Q9Y133	Q9y133 drosophila
6	1022.5	23.4	1305	5 Q9VPS7	Q9vps7 drosophila
7	1018.5	23.3	1305	5 Q9BML5	Q9bml5 drosophila
8	457	10.4	402	5 Q23442	Q23442 caenorhabdi
9	362.5	8.3	976	5 Q9V485	Q9v485 drosophila
10	343.5	7.9	983	11 Q62916	Q62916 rattus norv
11	342	7.8	879	11 Q9QYS2	Q9qys2 mus musculu
12	334.5	7.6	528	5 Q96954	Q96954 geodia cydo
13	330	7.5	872	4 Q9H3N6	Q9h3n6 homo sapien
14	330	7.5	977	13 Q9PWE1	Q9pwe1 ictalurus p
15	299.5	6.8	1188	13 Q9BUC5	Q9buc5 gallus gall
16	297.5	6.8	1242	13 Q9BUC4	Q9buc4 gallus gall
17	294.5	6.7	1156	13 Q9BUC6	Q9buc6 gallus gall
18	274.5	6.3	153	11 Q9QY85	Q9qy85 rattus norv
19	267	6.1	1199	11 Q9EPV6	Q9epv6 mus musculu

20	247.5	5.7	870	5	Q9N4T8	Q9n4t8 caenorhabdi
21	243.5	5.6	856	13	Q73638	Q73638 fugu rubrip
22	241.5	5.5	868	13	Q73636	Q73636 fugu rubrip
23	240	5.5	912	10	Q9C561	Q9c561 arabidopsis
24	237	5.4	877	13	Q9PW88	Q9pw88 carassius a
25	235	5.4	844	13	Q93552	Q93552 carassius a
26	231.5	5.3	738	5	Q9V4U3	Q9v4u3 drosophila
27	231.5	5.3	864	13	Q73637	Q73637 fugu rubrip
28	227	5.2	875	13	Q73640	Q73640 fugu rubrip
29	224.5	5.1	1056	13	Q9Y117	Q9y117 squalus aca
30	223	5.1	1055	13	Q9YGW3	Q9ygw3 oryzias lat
31	222	5.1	1055	13	Q98U11	Q98u11 oryzias lat
32	219.5	5.0	848	13	Q93553	Q93553 carassius a
33	219	5.0	941	10	Q9SWD9	Q9swd9 arabidopsis
34	212	4.8	1267	5	Q93564	Q93564 caenorhabdi
35	211.5	4.8	925	10	Q65498	Q65498 arabidopsis
36	211.5	4.8	962	10	Q23048	Q23048 arabidopsis
37	209	4.8	1070	13	Q93490	Q93490 anguilla ja
38	207	4.7	808	11	Q35190	Q35190 mus musculu
39	202.5	4.6	880	13	Q73639	Q73639 fugu rubrip
40	201.5	4.6	912	10	Q9SES5	Q9ses5 brassica na
41	195	4.5	843	11	Q9Z0R7	Q9z0r7 rattus norv
42	193.5	4.4	551	13	Q9PWQ0	Q9pwq0 fugu rubrip
43	190.5	4.4	923	10	Q9ZV68	Q9zv68 arabidopsis
44	189.5	4.3	953	10	Q9ZV67	Q9zv67 arabidopsis
45	187	4.3	502	13	Q98845	Q98845 anguilla ja

ALIGNMENTS

RESULT 1

Q9BML7	PRELIMINARY;	PRT;	840 AA.
ID	Q9BML7		
AC	Q9BML7;		
DT	01-JUN-2001 (Tremblrel. 17, Created)		
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)		
DE	01-JUN-2001 (Tremblrel. 17, Last annotation update)		
DE	METABOTROPIC GABA-B RECEPTOR SUBTYPE 1.		
GN	GABA-B-R1.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	PubMed-11168554;		
RA	Mezler M., Muller T., Raming K.;		
RT	"Cloning and functional expression of GABA-B receptors from		
RL	Drosophila."		
RL	Eur. J. Neurosci. 13:477-486(2001).		
DR	EMBL; AF318272; AAK13420.1; .		
KW	Receptor.		
SQ	SEQUENCE 840 AA; 94384 MW; C091A9F406C97500 CRC64;		

Query Match	100.0%;	Score 4374;	DB 5;	Length 840;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 840;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MRKDMTSDGATFWIFLLCLIASPHLQGGVAGRPDELHIGGIFFIAGKGGWGGQACMPA	60	
Db	1	MRKDMTSDGATFWIFLLCLIASPHLQGGVAGRPDELHIGGIFFIAGKGGWGGQACMPA	60	
QY	61	TRLALDDVNNKPNLLPGFKLILHSNDSCEPGLGASVMYNNLYNKPQKLMLLAGCSTVCT	120	
Db	61	TRLALDDVNNKPNLLPGFKLILHSNDSCEPGLGASVMYNNLYNKPQKLMLLAGCSTVCT	120	
QY	121	TVAAAKMWNILVICYGASSPALSDDRFPPLFRTHPSATVHNPTRIKLMKKFGSRAI	180	
Db	121	TVAAAKMWNILVICYGASSPALSDDRFPPLFRTHPSATVHNPTRIKLMKKFGSRAI	180	

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QY 181 LQAAEEVFISTVEDLENRCMEAGVEIVTROSFLSDPTDAVNRRLRQDARIIVGLFYVVA 240
Db 181 LQAAEEVFISTVEDLENRCMEAGVEIVTROSFLSDPTDAVNRRLRQDARIIVGLFYVVA 240
QY 241 RRVLCEMYKOOLYGRAHVWFIFIGWYEDNMYEVNKAEGITCTVQMRIRAAEGLHTTEALM 300
Db 241 RRVLCEMYKOOLYGRAHVWFIFIGWYEDNMYEVNKAEGITCTVQMRIRAAEGLHTTEALM 300
QY 301 WNQNNQTTISGMTAEFRHRLNQAALIEEGYDINHRYDPEGYQEAFLAYDAVWSVALAFNK 360
Db 301 WNQNNQTTISGMTAEFRHRLNQAALIEEGYDINHRYDPEGYQEAFLAYDAVWSVALAFNK 360
QY 361 TMRLLTTGKSLRDFYTDKDEIADEIYAAMNSTQFLGSGVWFAESSQGDRIALTQIOMI 420
Db 361 TMRLLTTGKSLRDFYTDKDEIADEIYAAMNSTQFLGSGVWFAESSQGDRIALTQIOMI 420
QY 421 DGKYEKLGYYDTOLDNLWSLNTQEWIGGKVPQDRTIYTHVLRVTSVLPFLVCMCTISSCGI 480
Db 421 DGKYEKLGYYDTOLDNLWSLNTQEWIGGKVPQDRTIYTHVLRVTSVLPFLVCMCTISSCGI 480
QY 481 FVAFALIIFNWNKRRVIOSSHVPVCNTIMLFGVILICLSVILGIDGRFVSPPEYPRKIC 540
Db 481 FVAFALIIFNWNKRRVIOSSHVPVCNTIMLFGVILICLSVILGIDGRFVSPPEYPRKIC 540
QY 541 QARAWLLSTGFTLAYGAMFSKVRVHRFTTKAKTDPRKKVPEWPKLYTWMSGLLSIDLVIL 600
Db 541 QARAWLLSTGFTLAYGAMFSKVRVHRFTTKAKTDPRKKVPEWPKLYTWMSGLLSIDLVIL 600
QY 601 LSWQIFDPLQRYLETPLDPVSTDDIKIRPELHESORNSMWGLVYFGKLLVFG 660
Db 601 LSWQIFDPLQRYLETPLDPVSTDDIKIRPELHESORNSMWGLVYFGKLLVFG 660
QY 661 LFLAYETRSIKVQINDSRVYVGSIIYNNVVLCLITAPVGMVIAEQDASFAFVALAVIFC 720
Db 661 LFLAYETRSIKVQINDSRVYVGSIIYNNVVLCLITAPVGMVIAEQDASFAFVALAVIFC 720
QY 721 CFFLSMLLIFFPKVIEVIRHPKDAESKYNPDSSAISKEDEERYQKLVTEQOLRLITQKE 780
Db 721 CFFLSMLLIFFPKVIEVIRHPKDAESKYNPDSSAISKEDEERYQKLVTEQOLRLITQKE 780
QY 781 EKIRLVRQRLVERGDAGTELNGATGVASAAVATTSOPASLINSAAHTPAATLAIQTGE 840
Db 781 EKIRLVRQRLVERGDAGTELNGATGVASAAVATTSOPASLINSAAHTPAATLAIQTGE 840

RESULT 2
Q9V309 PRELIMINARY; PRT: 1713 AA.
AC Q9V309;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CG15274 PROTEIN.
GN GABA-B-R1 OR EG:DS00929.6 OR CG15274.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutcliffe G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Beriman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.B., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, AND CN BW SP;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R.G., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
RA Celniker S., Rubin G.M.;
RT "An exploration of the sequence of a 2.9-Mb region of the genome of
Drosophila melanogaster: the Adh region."
Genetics 153:179-219(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, AND CN BW SP;
RA Celniker S.E., Aghayani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA Butenhoff C., Champagne M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.L., Rubin G.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE003646; AAF53431.1; -.
DR EMBL: AE003411; AAF4910.1; -.
DR FlyBase: FBgn0028924; GABA-B-R1.
DR InterPro: IPR001828; ANF receptor.
DR InterPro: IPR000337; GPCR_Mgr.
DR InterPro: IPR000402; Na_K_beta.
DR Pfam: PF000003; 7tm_3; 1.
DR Pfam: PF01094; ANF_receptor; 1.
DR Pfam: PF00287; Na_K-ATPase; 1.
DR PROSITE: PS0259; G_PROTEIN_RECEP_F3_4; 2.
KW Hypothetical protein.
SQ SEQUENCE 1713 AA; 195133 MW; 8474EBC5F9FA27AC CRC64;
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Query Match 75.8%; Score 3317; DB 5; Length 1713;

Best Local Similarity 45.0%; Pred. No. 7.3e-251;

Matches 737; Conservative 16; Mismatches 19; Indels 866; Gaps 10;

QY 3 KDMTSDGAVTFWIFLCLITASPHLOGGVAGRPDELHIGGIFPIAGKGGWOGQACMPATR 62

Db 142 RDMTSDGAVTFWIFLCLITASPHLOGGVAGRPDELHIGGIFPIAGKGGWOGQACMPAAR 201

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Qy 63 LALDDVNKOPNLLPGFKLILHSNDECEPGLGASVWYNLLYNKPKMLLAGCSTCTTV 122
Db 202 LALDDVNKOPNLLPGFKLILHSNDECEPGLGASVWYNLLYNKPKMLLAGCSTCTTV 261
Qy 123 AEAAMWNLIVLCYGASSPALSDDRFRFPFLFTHPSATVHNPTRIKLMKKFGSRVAILQ 182
Db 262 AEAAMWNLIVLCYGASSPALSDDRFRFPFLFTHPSATVHNPTRIKLMKKFGSRVAILQ 321
Qy 183 QAEVFIISTVDELENRCMEAGVEIIVTROSFLSDPTDAVRLRRQDARIIVGLFYVVAAR 242
Db 322 QAEVFIISTVDELENRCMEAGVEIIVTROSFLSDPTDAVRLRRQDARIIVGLFYVVAAR 381
Qy 243 VLCEMYKOOLYGRAHWFFIGHYEDNWVEYNLKAEGITCTVEOMRTAAEGHLLTTEALMN 302
Db 382 VLCEMYKOOLYGRAHWFFIGHYEDNWVEYNLKAEGITCTVEOMRTAAEGHLLTTEALMN 441
Qy 303 ONNOTTISGMTAEER-----RHRLNOALIEEGYDINHRYPEGY 341
Db 442 ONNOTTISGMTAEERVLVLLYPLKFLLOCAFFLRHRLNQALIEEGYDINHRYPEGY 501
Qy 342 QEAPLAYDAVMSVALAFNKTMBRLTGTGKSLRDFYTDKEIADEIYAAMNSTQFLGVSGV 401
Db 502 QEAPLAYDAVMSVALAFNKTMBRLTGTGKSLRDFYTDKEIADEIYAAMNSTQFLGVSGV 561
Qy 402 VAFSSQGBRIALTQTEQMIDGKYEKLGYDQDNLNLSWLNTEQWIGGK-----449
Db 562 VAFSSQGBRIALTQTEQMIDGKYEKLGYDQDNLNLSWLNTEQWIGGKTKHVTTPNKN 621
Qy 450 -----449
Db 622 GNPSSQDVTNRGSLTSLSEKNDKSNPSSASLOQAPKVAPKPKLSISDAGKDTVTQKV 681
Qy 450 -----449
Db 682 KENEPGFSKOFKESIGVRANRNSATKKENEKLLVKTVPKSLIKESNDENVEPSRRT 741
Qy 450 -----449
Db 742 KSQPVGKKVYEESTRVRPEPDSFDREKLYSDMIDYDRSSDVPPEKLSWEPDSTLRRR 801
Qy 450 -----VPO-----452
Db 802 FVSNEXHSSLEGEEDLDLDSVGSSTMRGYSYRMPQNAEDERPVLIAELINMGKELKE 861
Qy 453 -----DRTI-----VTHV-----460
Db 862 QRESTNVRNRRDKTIDEVKGSKIITGSKOHVEEVKYNETASNEDDDNAQVKHIGTIT 921
Qy 461 -----460
Db 922 KIFSTIAORMKEKSSSEEDENKDNKDKDKDKDBQKLPPPEIELEAKKAWTPI 981
Qy 461 -----460
Db 982 AETSPDIPGENQILQEQYQKVGKIGKRNKRYCIGINTDISRKSKITFISKSAGDGLVYH 1041
Qy 461 -----LRTVSLPLFV-----470
Db 1042 DGGRLRDIGQTENLKNORKNHHKHTEPDIPVDIGHSDRVRTEIGVNTKPLPIIPI 1101
Qy 471 -----470
Db 1102 AEMHVHNGKLRDICTGTDKFPWIDDDTDVLYMHPKTDKRLKLNKLIVDPDPDNGPYKM 1161
Qy 471 -----C-----MCTISSCGIFVAFALII 488
Db 1162 PTKEDRRTYYKGEVHFPGRTWRRLFFENKIHGKYKLRPSHWLTLVPSVLYILFVIIF 1221
Qy 489 FNW-----492
Db 1222 SNAWFDFIKDASRKVPKMKKAQPFISFTPIGRPTNPKAVSFDPRNSTEVMEKYAGIMAL 1281
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Qy 493 -----492
Db 1282 LEKYGDYGHNPFRFOTCTANKEFGYPSGEPVFLKVNRIIGFKTEPYINSDELVRKIDEV 1341
Qy 493 -----N 493
Db 1342 EFTALKRLLENTTTEEGHLNRTWTCRSDDKDKNVLIEPHPEPAIRTEYTDIEEKIEYIAN 1401
Qy 494 KHRR-----VTOSSHPVCNTIMLFGVILCLISVI 522
Db 1402 EGKKSFFGPNVDNRIVALKIKNLKANERVHINCKIIVIQSSHVPVCNTIMLFGVILCLISVI 1461
Qy 523 LLGIDGRFVSPPEYPKICQARAWLLSTGFTLAYGAMFSKVVRHFTTKAKTDPKKKVEP 582
Db 1462 LLGIDGRFVSPPEYPK-----1477
Qy 583 WKLYTMVSGLLSIDLVILLSMQIFDPLQRYLETPELPEDVPSTTDDIKIRPELEHESORN 642
Db 1478 -----IFDPLQRYLETPELPEDVPSTTDDIKIRPELEHESORN 1515
Qy 643 SMWGLVYGFKGLJLVFLGFLAYETRSIKVKQINDSRVYVMSIYVNVVLCITAPVGMVI 702
Db 1516 SMWGLVYGFKGLJLVFLGFLAYETRSIKVKQINDSRVYVMSIYVNVVLCITAPVGMVI 1575
Qy 703 ASQODASFAVALAVIFCCFLSMILLIFVPKVIIEVIRHPKKAESKYNPDPSAISKEDEERY 762
Db 1576 ASQODASFAVALAVIFCCFLSMILLIFVPKVIIEVIRHPKKAESKYNPDPSAISKEDEERY 1635
Qy 763 QKLVTENEQRLQRLTOKEEKIRVLRQRLVERGDAGKTELNGATGVASAAVATTSQPASLI 822
Db 1636 QKLVTENEQRLQRLTOKEEKIRVLRQRLVERGDAGKTELNGATGVASAAVATTSQPASLI 1695
Qy 823 NSSAHATPAATLAIQTGE 840
Db 1696 NSSAHATPAATLAIQTGE 1713
RESULT 3
Q9N502 PRELIMINARY; PRT; 816 AA.
AC Q9N502;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Y41G9A.4 PROTEIN.
GN Y41G9A.4
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RL investigating biology. The C. elegans Sequencing Consortium. ";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Ryan E., Wohlman P., Walker C., Fielder T.;
RT "The sequence of C. elegans cosmid Y41G9A.4";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Waterston R.;
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC006761; AAF60549.1; -.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
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DR Pfam: PF01094; ANF_receptor; 1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3.4; 1.
SQ SEQUENCE 816 AA; 92251 MW; 4363D11A46CBECA1 CRC64;

Query Match 39.9%; Score 1746.5; DB 5; Length 816;
Best Local Similarity 46.4%; Pred. No. 3.7e-128;
Matches 356; Conservative 131; Mismatches 251; Indels 29; Gaps 11;

QY 46 AGKGWGGGACMPATRIALDDVKNQPNLLPGFKLIHNSDCEPGLGASVYNNLYNK 105
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 106 POKMLLAGCSTVCTVTAEEAAKMWNLVLVLCYGASSPALSDDRKRFPFLFRTHPSATVHNPT 165
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 166 RIKLKKFGWSVAILOAAEVEFISTVEDLENRCMEAGVEIVTQSFSLDPTDAVNLRR 225
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 123 RIHIMEKPKRFTILMSVEEVFTAKDLEAIAARKGKIK-VDRQSYFGDPTDAMKTQR 181
QY 226 QDARIIVGLVYVAARRVLCMEYKQOLYGRAHWFFIGVYEDNMYEVNLKAEGITCTVEQ 285
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 192 QDARIIVGLVYVTEARKVLCQAYHGLYGRYVWFIFGYADTWY-IPPEEHLNCTAEQ 240
QY 286 MRIAEGHLLTTEALMWNQNTTISGMTAEFRHRLNQALIEGYDINHDRVPEGYOEAP 345
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 MTEAEAYHFTTESVMSLRDNPISAMTGMQFOQLTQYFQDANVG-----GFPEAP 294
QY 346 LAYDAVSVAFANFTMERLTTGKSLRDTYTDKEIADEIYAAMNSTOFLGVSGVVAFS 405
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 295 LAYDAVVALAFNCTRNRLPSHIR-LENFTYDNKVIADTLFOCVKNTSPRGVSGVMFS 353
QY 406 SOGDRIALTOIEQMDGKYEKLYGYDTQDNLNLSWLNTEQWIGK-VPODRTIVTHVLRV 464
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 354 DSGDRIARTQIEQMOGGKYMIGYDITTSGLDEWYNKEQWLNKGPPPOSTVTKKHAMTV 413
QY 465 SLPFVCMCTISSCGIFVAFALIIFNWNKRRVIOSSHPPVCNTIMLFGVILCLISVILL 524
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 414 SNEFYPTLFAVLGAACVFIYFQKHHERLIIFQSQPECNNILLIGCSLCFLSLFLI 473
QY 525 GI--DGRFVSPEYKPKIOARAWLSTGTFLAYGAMFSKVRVHRF--TTKAKTDPKKKV 580
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 474 GLPDDDISISLFLPCLLCHARVITLLFGFTFYAGSFAKVIIVHRMGATENQQLASRQKD 533
QY 581 EP--WKLYTWVSGLLSIDLVILLWSQIFDPLQRYLETETPLEDPVSTTDIKIRPLEHC 637
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 534 EPISSKFFVIVAAULTAVDVFCVFWVLIDPLHLTEQKPLFTPADSEDEMIPLVLCQ 593
QY 638 ESQRNSMVLGLVYKGLILVFLGLFLAYETRSIKVRQINDSRVYVMSIYNNVVLCLITAP 697
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 594 QSNQOEQVWGIIMGPKLLVFGTFLSYETRNLLKRFINDSRVGLAIYNNVAVMTLVTP 653
QY 698 -VGMVIAOODASFAFVALAIFCCFLSMILLIFVPKVIEWIRHPKDAESKYNPD---SA 753
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 654 VVTLTHGKVDANFANFISLTV-----GLIYGPRIHIIKVPSPSADEIQLNGNVPGV 705
QY 754 ISKEDEERYQKLVTEQQLRTOKEEKIRVRLRQLVERGDAGKTE 800
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 706 MSKVQDKRYDMLKKENETLOIQIEEKRIHECKERLEELTKNSET 752

RESULT 4
QY 09BML6 PRELIMINARY; PRT: 1220 AA.
AC Q9BML6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE METABOTROPIC GABA-B RECEPTOR SUBTYPE 2.
GN GABA-B-R2.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11168554;
RA Mezler M., Muller T., Raming K.;
RT "Cloning and functional expression of GABA-B receptors from
RT Drosophila.";
RL Eur. J. Neurosci. 13:477-486(2001).
DR EMBL; AF318273; AAK13421.1; .
KW Receptor..
SQ SEQUENCE 1220 AA; 137976 MW; 2B33DA2C1A1BDA8B CRC64;

Query Match 27.1%; Score 1186.5; DB 5; Length 1220;
Best Local Similarity 32.9%; Pred. No. 5.8e-84;
Matches 272; Conservative 183; Mismatches 311; Indels 61; Gaps 23;

QY 17 LLCILIASPHLQGGVAGRPDELHIGGIPIA-GKGGWGGQACMPATRIALDDVKNQPNLL 75
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 12 LFLLLWSTACGRTAKRSD-VYIAGFFPGDVENSYTGRCVMPSVKLALGHVNEHGKIL 70
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 76 PGFKLIHNSDSECEPGLGASVMTNNLYNKPKQLMLL-AGCSTVCTTVAAEAAKMWNLVL 134
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 71 ANYRLHMMWNDTQCNAAVGVKSFDFDMMHSGPNKVMFLGCACTHTVDPITAKASKHMLTQL 130
QY 135 CYGASSPALSDDRKRFPFLFRTHPSATVHNPTRIKMKFGWSVAILOAAEVEFI---S 190
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 131 SYADTHPMFT-KDAFPNFFRVVPSENAFNAPRLALLKEFNWTRVGTVFQNEPRSLPHNH 189
QY 191 TVELENRCMEAGVEIVTQSFSLDPTDAVNLRRQDARIIVGLFYVVAARRVLCMEYKQ 250
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 190 MVADLD--AME--VEVVTQSFVNDVAESLAKLKVRIILGNFNEHFARKAFCEAYKL 245
QY 251 QLYGRAHWFFIGVYEDNMYEVNLKAEGITCTVEQMTAAEGHLLTTEALMWNQNTTIS 310
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 246 DMVGRAYQWLIMATYSTDMWNVTDQSE---CSVEEIALEGAILVLLPLSTSGDITVA 302
QY 311 GMTAEFRHRLNQALIEGYD---INHDYPEGVQEAFLAYDAVSVAFANFTMERLT 366
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 303 GITADEY-----LVE--YDLRGTEYSRF-HGY-----TYDGIWAAALAIQYVAEK-- 345
QY 367 TGKSLRDTYTDKEIADEIYAAMNSTOFLGVSGVVAFSQGDRIALTOIEQMDIGKYER 426
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 346 -REDLLTHFDYRVKDWESVFLAELRNTSFEVGTGPVRYN-NERRKANILINQFQLGOMEK 403
QY 427 LGYDTQLD--NLSWLNTEQWIGKVPQDRTIVTHVLRFTVSLPFCVMCTISSCGIFVAF 484
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 404 IGEYHSQKSHLDLSLGRPKVWVGKTPPKDRTLIYIHSQVNPITYIVSASASVIGVITAT 463
QY 485 ALIIFNWNKRRVIOSSHPPVCNTIMLFGVILCLISVILLIGDGRFVSPEEYKPKIOARA 544
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 464 VFLAFNIRKYNQRIKMSPPHNLNLIIVGCMITLUSIIFLGLDPTLSSVAAPPYICTARA 523
QY 545 WLLSTGFTFLAYGAMFSKVRVHRFTTKRQDTPKKVPEWPKLYTWVSGLLSIDLVILLSWQ 604
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 524 WILMAGFSLSGAMFSKWTWRVHSIFTDLKLN-KVKIKDYQLFMVGVLLAIDIAITITWQ 582
QY 605 IFDPLQRYLETETPLEDPV--STDDDIKIRPELEHCEQSQRNSMVLGLVYFGKLIILVFLG 662
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 583 IADPF--YRETQKLE-PLHHEINDDVLVPIPENEYCQSEHMTIFVSIYAYKGLLVFGAF 639
QY 663 LAYETRSIKVRQINDSRVYVMSIYNNVVLCLITAPVGMVIAOODASFAFVALAIFCCF 722
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 640 LAWETRHVSIPALNDSKHIGFSVNVFITCLAGAAISLSDRKDLVFLVLSFFIIFCTT 699
QY 723 LSMILLIFVPKVIEWIRHPKDAESKYNP-----DSAIKSEDEERYQKLVTEQ 771
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 700 ATCLCLVFPKLVKELKRNQGVVDRKVRATLRPMKNGRDRSSVC-ELQRLRDRVNTNCR 758
QY 772 LQRLITQKEEKIRVRLRQLVERGDAGKTELNAGTAVSAVAATTSQP 818
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db 759 FRKALMERENELQALIRKL---GPEARKWIDGVTCTGGSNVSGSELEP 802

RESULT 5

Q9Y133 PRELIMINARY; PRT; 1221 AA.

AC Q9Y133;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE BCDNA:GH07312 PROTEIN.

GN GABA-B-R2 OR BCDNA:GH07312 OR CG6706.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RX MEDLINE=20196006; PubMed=107311132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Ananadides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Doolittle R., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foslter C., Gabriellian A.C., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleby J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

[2]

RP SEQUENCE FROM N.A.

RA Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,

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RA Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,

RA Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,

RA Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleby J.M.,

RA Park S., Sequeira A., Sethi H., Snir E., Svirkas R.R., Weinburg T.,

RA Celniker S.E.;

RT "Full length Drosophila melanogaster cDNA sequence.";

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE003736; AAF55916.1; -;

DR EMBL; AF145639; AAD38614.1; -;

DR FlyBase; FBgn0027575; GABA-B-R2.

DR InterPro: IPR001828; ANF_receptor.

DR InterPro: IPR000337; GPCR_Mgr.

DR Pfam: PF00003; 7tm_3; 1.

DR Pfam: PF01094; ANF_receptor; 2.

DR PROSITE: PS0259; G_PROTEIN_RECEP_F3_4; 1.

SQ SEQUENCE 1221 AA; 138123 MW; A57A9954F31FOA05 CRC64;

Query Match 27.1%; Score 1183.5; DB 5; Length 1221;

Best Local Similarity 32.8%; Pred. No. 9,9e-84;

Matches 271; Conservative 184; Mismatches 311; Indels 61; Gaps 23;

QY 17 LLCLIASPHLOGGAGRPDELHIGGIPIIA-GKGGWGGQACMPATRLALDDVKNQPNLL 75.

DB 12 LLFLLMSTACGRATKRS-DVYIAGFFPYGDGVNSYTGRCMVSVKLALGHVNEHGKL 70

QY 76 PGFKLILHSNDSCEPGIGASVMYLNLYNKPQKLMLL-AGCSTVCTTVAEAAKMNLLVL 134

DB 71 ANYRLHMWNDOCNAAAVGVKSFEDMHSGPNKVMYLFGAACHTVTDPIAKASKRHHULTQL 130

QY 135 CYGASSPALSDRKRFPTLFRTHPSATVHNPTRIKLMKFGWSRVAILQQAAEEVFI----S 190

DB 131 SYADTHPMFT-KDAFPNFFRVVPSSENAFNAPRLALLKEFNWTRVGVYVQNEPRYSLPHNH 189

QY 191 TVDELNRCMEAGVEIVTROSFLSDPTDAVNLRRQDARIIVGLFVYVAARVCEMYKQ 250

DB 190 MVADLD--AME--VEVYETQSFVNDVAESLKLREKDVRIILGNFNEHFARKAFCEAYKL 245

QY 251 QLYGRAHVWFEGWYEDNNWVENLKAEGICTVTEOMRTAAEGHLLTTEALMNNQNTTIS 310

DB 246 DMYGRAYQLIMATYSYDWMNVOTDSE---CSVEIATALEGAILVDLLPLUSTSGDITVA 302

QY 311 GMTAEFRHRLNALIEEGYD---INHDRYPEQZAPLAYDAVWSVALFNKTMERLT 366

DB 303 GITADEY-----LVE--YDLRGTEYSRF-HCY-----TYDGIWAALAIQYVAEK-- 345

QY 367 TGKKSURDFTYKEIADEIYAAMNSTQFGLGVGVAFSSQGDRIALTQTEQMDTGKYEK 426

DB 346 -REDLLTHFDYRVKDWESVLEALRNTSFEVGTGVPVRYN-NERKANILINQFOLGOMEK 403

QY 427 LGYDQTDLD--NLSWLNTEQWIGKVPQDDRTIVTHVLTSLPLFCVCMCTISSGIGIVAF 484

DB 404 IGEYHSQKSHLDLSLGLKPVKRWGKTPPKRDLIYIEHSQVNPNTIYIVSASVIGVIAT 463

QY 485 ALIIFINWKNRRVIOQSHHPVCNTIMLFGVILICLISVLLIDGRFVSPEYPRKICQARA 544

DB 464 VFLAFNLYKYNQRYIKMSPHLNNLIIVGCMNTYLSIFLGLDITLSSVAAPFICTARA 523

QY 545 WLLSTGFTLAYGAMFSKVRVHRFTTKAKTDPKKKVPWKLYTWVSGLLSIDLVILLSWQ 604

DB 524 WILMAGFSLSGAMFSKTRVHSIFTDLKLN-KVKIDYQLFMVGVVGLAIDIAIITWQ 582

QY 605 IFDPLORYLETFPLEDPV--STDDDKIRPELEHCEQSQRNSWGLVYGFKGLLIVFGLF 662

DB 583 IADPF--YRETKOLE-PLHHENIDDLVIVPENECYQSEHMTIFVSIYAYKGLLVFGAF 639

QY 663 LAYETSIKVKQLNDSRYVGMISYVNVVLCILITAPVGMVIAEQDASQAFVALAVIFCCF 722

DB 640 LAWETHRVSPALNDSKHIGFSYVNVFITCLAGAAISLVLSDRKDLVFLVLSFIEICTT 699

QY 723 LSMLLIFVPKVIIEVIRHPKDKAESKYNP-----DSAIKDEDEERYQKILVTNEQ 771

DB 700 ATCLLVFPKVLKRNPOGVKRVKRVKATLRPMKSKNGRRDSSVC-ELEQRLRDVKNCR 758

QY 772 LQRLITQKEKIRVLRORLVERGDAKTELNGATGCVASAAVATTSQP 818

DB 759 FRKALMERENELQALIRKL---GPEARKWIDGVTCTGGSNVSGSELEP 802

RESULT 6

Q9VPS7 PRELIMINARY; PRT; 1305 AA.

ID Q9VPS7;

AC Q9VPS7;

DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE CG3022 PROTEIN.
 GN GABA-B-R3 OR CG3022.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
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 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
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 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
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 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
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 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RL "The genome sequence of Drosophila melanogaster.";
 SC Science 287:2185-2195(2000).
 DR ENBL: AE003588; AAF51465.2;
 DR FlyBase: FBgn0031275; GABA-B-R3.
 DR InterPro: IPR001828; ANF_receptor.
 DR InterPro: IPR000337; GPCR_Mgr.
 DR InterPro: IPR000005; HTHarac.
 DR Pfam: PF00003; 7tm3; 1.
 DR Pfam: PF01094; ANF_receptor; 1.
 DR PRINTS: PR00248; GPCRMR.
 DR PROSITE: PS0259; G-PROTEIN_RECEPTOR_F3_4; 1.
 DR PROSITE: PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
 SQ SEQUENCE 1305 AA; 143588 MW; A9C3C85307650450 CRC64;

Query Match 23.4%; Score 1022.5; DB 5; Length 1305;
 Best Local Similarity 29.1%; Pred. No. 4.7e-71;
 Matches 250; Conservative 171; Mismatches 348; Indels 91; Gaps 22;

QY 41 GLEPTA-KGGGQGGACMPATRLALDDVKNQPNLLPGFKLLHNSDSECEGLGASVMY 99
 DB 157 GLFELSTGRPRDGLSELGAATMAVEHNRK-RLPGYTLLELVNTDQCDCGVGDVDRFF 215

QY 100 NLLYNPKQKMLL--AGCSTVCTTVAEAAKMNWNLVLCYGASSPALSDRRKRPFTLFRTH 156
 DB 216 HAIYQPTSTRVWMLLGSACESEVTEAKVYVYWNIVOVSGFSTSPALSDRRFPYFTRTV 275
 QY 157 PSATVHNPTRIKLMKFGWSRVAILQAAEEVFISTVEDLENRCMEAGVEIVTOSF-LSD 215
 DB 276 APDSSHNPARIAIRKFGWGTVTTFSSONEEVHSLAVNNLVTELEAANISCAATITFAATD 335
 QY 216 PTDVAVNRLRQDARIIVGLFVYVAARVLCMEYKQQLYGRAHVWFF-----IGWYENWY 270
 DB 336 FKEQLLLLRTRTDRIIIGSFQSLEAPQILCEAYRLRMFGADYAWILHESMGAPWPD--- 392
 QY 271 EVNLKAGITCTVEOMRIAAEGHLLTALMWNQNNOTTISGMTAEFRHLNQAALIE--- 327
 DB 393 -----QRTACSNEHQLAVENLIVSTHNSIVGNNSYSGLNNHMFNSLQKSOAFHG 446
 QY 328 -----EGY-----DINHNR-----YPEGY-QEAPLAYDAVMSVALAF 358
 DB 447 QDGFSGYSGRISIAATQSDSRRRRRRGVGTSGHLFPEAISQYAPQTYDAVVAIALAL 506
 QY 359 NKTME--RLPTGKSLRDFTYTDKEIADEIYAAMNSTQFLGVSGVWAFSSQGDRIALTQI 416
 DB 507 RAAEEHWRNREEQSKLDGFDYTRSDMAWEFLQOMGKLHFLGVSGVPVSFGP-DRVGTTF 565
 QY 417 EQMIDGKYELGYDITOLDNLW----LNTQWIGGKVPQDRTIVTHVLRVSLPLFCVM 472
 DB 566 YQORGLEVALYYPATDALDFRCPRPVKWHSGQVPIAKRVFKLRVATIAPLAFYTI 625
 QY 473 CTISSCGIFVAFALIIENINKHRRVIOSSHPCVNTIMFGVILICLSVILLGIDGRFV- 531
 DB 626 ATLSVGIALAIAFLAENLHFRKKAIKLSPKLSNITAVGCCIFVATVILLGDHSTLP 685
 QY 532 -SPEEYKICQARAWLLSTGFTLAYGAMFSKVRVHR-FTTKAKTDPKKKVEPKWKLXTMV 589
 DB 686 SAEDSPATVCTARVYLLSAGSLGAFSGMFAKTYRVHRTFTRTGVSVEFKDKMLQIQLILV 745
 QY 590 SGLSLDLVILLSWQIFDPLQRYLETPLDPVSTTD-DIKIRPELEHCEQSQRMSMIGL 648
 DB 746 GGLLLDALLVTLVWVVDPMERHLNLTLE--ISATDRSVVYQPVQVEVCRSQTWLSV 803
 QY 649 VYCFKGLILVGLFLAYETRSIKVKQINDSRVGMISYVNVVLCITAPVGMVITASQDA 708
 DB 804 LYAFKGLLLVGVVYVMWETVRHVKIPALNDSQYIGVSVISVITSAIVVVLNLSERVTL 863
 QY 709 SFAFVALAVIFCCPLSMLLIFFVPR-----VIEWIRHPKDKAESKYNPDSAISKEDE 759
 DB 864 AFITITALITSTATLCLLFIPLKLDIWARNDIIDPVIHSMG-LKMECNTRRFVVDRR 922
 QY 760 ERYOKLVTEQELQRLTQKEEKTIRVLRQRLVERGDAGKTELNGATGVASAATTSQPA 819
 DB 923 ELQYRVQVQNRVYKKEIQALDAEIRKL-ERLLESG-----LTTTSTTSST 968
 QY 820 SLINSSAHATPAATLAIQOG 839
 DB 969 SLTTGGGHLRP--ELTVISG 986
 RESULT 7
 QYBM15 PRELIMINARY; PRT; 1305 AA.
 ID QYBM15
 AC QYBM15
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE PUTATIVE METABOTROPIC GABA-B RECEPTOR SUBTYPE 3.
 GN GABA-B-R3.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.

RX PubMed-11168554;
RA Mezler M., Muller T., Raming K.;
RT "Cloning and functional expression of GABA-B receptors from
RL *Drosophila*.";
RL Eur. J. Neurosci. 13:477-486(2001).
KW EMBL; AF318274; AAK13422.1; -;
SQ SEQUENCE 1305 AA; 143701 MW; 8BBFA80F0E9BEADD CRC64;

Query Match 23.3%; Score 1018.5; DB 5; Length 1305;
Best Local Similarity 29.0%; Pred. No. 9.7e-71;
Matches 249; Conservative 171; Mismatches 349; Indels 91; Gaps 22;

QY 41 GIPPIA-GKGGWGGQACMPATRIALDDVKNQPNLLPGFKLIHNSDSECEPLGASVMY 99
Db 157 GLFELSTRGPRPDGLSELGAATMAVEHNRK-RLLPGYTLELVNTDQCPGVGVDFREF 215
QY 100 NLLYKPKQKMLL---ACGSVCTTVAEAKMWNLLVLCYCGASSPALSDDKRPFTLFRTH 156
Db 216 HAIYQPTSTRVMMLLGSACSEVTESLAKVPVYNNIVQVSFGSTSPALSDDKRPFTLFRTH 275
QY 157 PSATVHNPTRIKMKKFGWSRVAILQQAEEVFISTVEDLENRCMEAGVIVTRQSF-LSD 215
Db 276 APDSSHNPARIAIRKFGVGTTFQSONEEVHSLAVNNLVTELEAANISCAATITFAATD 335
QY 216 PDAVNRNRDARIIVGLFYVAARRVLCEMYKOOLYGRAHWFF-----IGWYEDNNY 270
Db 336 FKEQLLLRRTDTRIIIGFSQELAPQILCEAYLRMFCADYAWILHESMGAPWPD--- 392
QY 271 EVNLKAEGITVQEMRTAAEGHLLTEALMNQNTTISGMTAEFRHRLNQALIE--- 327
Db 393 -----QRTACSNHELQLAIVENLIVVSTHNSIVGNVSYSLNNHMFNSQLRKSQAQFHG 446
QY 328 -----EGY-----DINHDR-----YPEGY-QEAPLAYDAVMSVALAF 358
Db 447 QDGFSGYGPRISTAATOSDERRRRRGVGTSGHGLPEALISQYAPQYDAVMAIALAL 506
QY 359 NKTWE--RLTTGKSLRFTYTDKEIADIYAAMNSTOFLGVGVVAFSSQGDRIALTOI 416
Db 507 RAAEEHRRNEEQSLKDFDTRSDMAWEFLQOMKHLFLGVGVPVFSFGP-DRVGTTF 565
QY 417 EOMIDGYEKLYDQDNLDSW----LNTQWIGGKVPQDRTIVTHVRLTVSLPLFVCM 472
Db 566 YQIQGGLLEPVALYPADALDFRCPRCPVKWHSQVPIAKRVFKLRVATLAPLAFYTI 625
QY 473 CTISGGLFVAFALIIFNWKHRRVIOSSHVPVNTIMLFGVILCLISVILLIGDGRFV- 531
Db 626 ATLSVGIALAITFLAFNLHFRKKAIKLSPEKLSNITAVGCFIVATVILLGLDHSHTLP 685
QY 532 -SPEEYPKICOARAWLLSTGTLAYGAMFSKVMVRVHR-FTTKAKTDPKKKVPEWKLTYMV 589
Db 686 SAEDSFATVCTARVYLLSAGSLAFSGMFAKTYRVHRIFTRTGSVFKDKMLQDIOILLV 745
QY 590 SGLSIDVILLVWQIFDPLQRYLETFFLEDPVSTTD-DIKIRPELHCEESORNMSWGL 648
Db 746 GGLLVLDALLVTLWVTDPMERHLLNLTLE--ISATDRSVYVQVQVRCRSOHTQTLVSV 803
QY 649 VYGFKGLILVGLFLAYETRSIKVQINDSRVGVMSIYNNVVLCLITAPVGMVIAQQDA 708
Db 804 LYAYGGLLVVWVYMWATREVRVKVLPALNDSQYIGVSVYSVWITSIVVLANLISERVTL 863
QY 709 SFAPVALAVIFCCFLSMILLIEVVK-----VIEVIRHPKDKAESKYNPDSAIKDE 759
Db 864 AFTITALILTSTATICLLPILPKLHDIWARNDIIDPVHSG-LKMECNTRFVVDDRR 922
QY 760 ERYOKLVTEENQRLITQKEEKIRVLQRVERGDAGKTELNGATGVASAAVATTSQPA 819
Db 923 ELQYRVVQNRVYKKEIQALDAEIRKL-ERLESQ-----LTTTSTTSST 968
QY 820 SLINSSAHATPAATLAIQ 839
Db 969 SLLTGGGHLKP--ELTTS 986

RESULT 8

Q23442 ID Q23442 PRELIMINARY; PRT; 402 AA.
AC Q23442;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE COSMID ZK180.
DE ZK180.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fulton L., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R., Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J., Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.;
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Pauley A., Le T.T.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U58748; AAB52965.1; -;
DR InterPro: IPR000337; GPCR_Mgr.
DR InterPro: IPR001064; Crystallin.
DR Pfam: PF00003; 7tm.3; 1.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE: PS00259; G_PROTEIN_RECEP_F3_4; 1.
SQ SEQUENCE 402 AA; 45577 MW; D48DF0916CB4EFEE CRC64;

Query Match 10.4%; Score 457; DB 5; Length 402;
Best Local Similarity 29.9%; Pred. No. 1.7e-27;
Matches 132; Conservative 74; Mismatches 161; Indels 74; Gaps 15;

QY 389 AMNSTOFLGVGVVAFSSQGDRIALTOIEQMIDGKYEKLYDQDNLNLSNLT--TEQWI 446
Db 15 AIDNSSFGLTGKVKFAN-NERLGLVDIKQWSDGQYVFAVDGADDEFKIIDSTTKGW- 72
QY 447 GGVPODRTIVTHVRLTVSLPLFVCMCTISSCGIFVAFALIIFNWKHRRVIOSSHVPC 506
Db 73 --SPPLDSTITERRRHHISILFLAM-----SILF-----IKMSSPNL 107
QY 507 NTMLFGVILCLISVILLGIDGRFVSPPEEYPKICOARAWLLSTGTLAYGAMFSKVMVRVH 566
Db 108 NNIIAGSICTFASVIMLGLDTRIVSPDVEFWLVCITWTLCIGTILSGFAMFSKTRWRV 167
QY 567 RFTTKAKTDPKKKVPEWKLTYMVSGLLSIDLVILLSHQIFDPLQRYLETFFLEDPVSTTD 626
Db 168 SIFTNTRMD-RKAIKDSKFLIIGILLFIDICVLVTFWAFVSPFS-YTVT---ELPHIPED 222
QY 627 DIKIRPELHCEESORNMSWGLVYGFKGLILVFLGFLFAYETRSIKVQINDSRVGVMSIY 686
Db 969 SLLTGGGHLKP--ELTTS 986

Db 223 NIVIIPEVEKCNSSHGVOAVLAVKGVLMILGCFLEWETRHVNVNVPALNDSKYIGTR-- 280
 QY 687 NVVVLCLITAPVGMVIAQQDASFAFVALVIFCCFL---SMLLTFVPKVIEVIRHPDK 743
 Db 281 -----TGQORDVQSRFV-----FCHFLDDTNVVSRCADSKFSKTPNFI 319
 QY 744 AESKYNPDSATSKEDK-----ERYQKLVTEQLORLITQKEKIRVLRLQBLVREGDAKTE 800
 Db 320 MKLEFN-----FSKNSYGGFKNFQKLSFGGFMIVFARSQVKKVIELARNPV-----GNE 369
 QY 801 LNG-ATGVASAAVATTSOPAS 820
 Db 370 PRAYRGLMKSVKATSPMS 390
 RESULT 9
 Q9V485 ID Q9V485 PRELIMINARY; PRT; 976 AA.
 AC Q9V485; 2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE GLU-RA PROTEIN.
 GN GLU-RA OR CG11144.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananatiades P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhang G., Zhao Q., Zheng L.,
 RA Yeh J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhou X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003846; AAF59402.1; -;
 DR FlyBase; FBgn0019985; Glu-RA.

DR InterPro: IPR001828; ANF_receptor.
 DR InterPro: IPR000337; GPCR_Mgr.
 DR Pfam: PF00003; 7tm_3; 1.
 DR Pfam: PF01094; ANF_receptor; 1.
 DR PRINTS: PR00248; GPCRMR.
 DR PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.
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Db 788 SOLYNM--ILITICIIYAIAKTRKIP-ENFESKFGFTWYTCIIWLAFPIYFGTNSY 844
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Db 845 EVQTTTLCISLSASVALCVLSPKVITLVPFP-DKNVRKLTMTNSTVYRRSAAVAQA 903
Qy 767 TENEOQLRIQKEKIRVLRORLVERGDAKTE-LNG---ATGVASAAVATTSQP---- 818
Db 904 PTSSGYSRT-----HAPGTSALTGGAVGTNASSSTLPTQNSPHLDE 944
Qy 819 ASLINSSAHAT 829
Db 945 ASAQTNVAHKT 955

RESULT 10
ID Q62916 PRELIMINARY; PRT; 983 AA.
AC Q62916;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 4b.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
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RA O'Hara P.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U47331; AAA88788.1; -.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR001828; ANF_receptor.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
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SQ SEQUENCE 983 AA; 109276 MW; 072F0D8B3A840A80 CRC64;
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Query Match 7.9%; Score 343.5; DB 11; Length 983;
Best Local Similarity 19.08; Pred. No. 5.6e-18;
Matches 170; Conservative 160; Mismatches 357; Indels 209; Gaps 35;

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Db 1 MSGKGGMAWMAWRLPLCLLLSLYAPWVPSLGGPKGHPHMSIRIDGDTLGLGPPVHGR 60

Qy 49 GWWGGGQAC-----MPATRLADVDNKNQNLPGFKL----- 80
Db 61 G--SEGKACGELKKEKGTHRLEAMFLDALRINDPDLPLNITLGARILDTCSDRTHALEQ 118

Qy 81 -----ILHNSDSECEPLGASVMYLLYKPKQLMLLAGC--STVCTTVAEAAKWNWL 131
Db 119 SLTFVRLAIKDGTEVRGSGGPP-----IITKPERVGVIGASGSVSTWVANILRLFKI 174

Qy 132 IVLVCGASSPALSQRKRPPTLFRTHPSATVTHNPTRIKLMKKGWSRVAIL-----QQA 184
Db 175 PQISYASTAPLSDNSRDFFSRVVPSTYQQAQAMVDIVRAIKWNVSTLASEGSGESG 234

Qy 185 EEVFTISTVEDLENRMEAGVEIVTRQSFLSDPTDAVRLNRDARIIVGLFVVAARRYL 244
Db 235 VEAFIQSRNGGVGCIQAQSVIPREPKTGEFDKIIKRLLETNSNARGIIFANEDDIRRYL 294

Qy 245 CEMYKQQLYGRAHWFFIGTWEDNW-----YEVNLAKEG-ITCTVEQMRITAAEGHLT 296
Db 295 EAARRANQTGH---FFWMG--SDSMGSKSAPVLRLEEVAEGAVTILPKRMSVRGDFRYS 349
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Qy 297 EALMWNQNNOTTISGMTAEPRHRLNOALIEEGYDI-----NHDRYPE--GYOE---APLA 347
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Qy 348 YDAVMSVALAFNKMTMERLTTGKSKSLRDTFTYDKEIADIEIYAAMNSTOFLGYSV--VVAFSS 406
Db 410 IDAVYANGHALHAMHRDLCPGRVGL--CPRMDPVDGTOLLKAYIRNVNFSGIAGNPVTENE 467
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Db 468 NGD-----APGRYD---IYQYQLRNGSABYKVGISWTDLHLHLRIERMOWPGSGQQ 514
Qy 452 QDRTIVT-----HVLRT----- 463
Db 515 LPRSICSLPCOPGERKKTVMGMACCWCEPCTGYQYQVDRYTCCTCPYDMRPTENRTSCQ 574
Qy 464 -----VSLPLFCMCTISSGIFAFALIFNIWNKHRRVIOSSHPCNTIM 510
Db 575 PIPVTKLENDSPWAVLPFLFVAVGIAAT-LFVVVTFVRYN----DTPIVKASGRELSVVL 629
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Qy 689 VVLCLTAPYGMVIAQQDASFAFV-----ALAVIFCCFLSMLLIFVPKIVIEVIRH 739
Db 795 CIVWLAFIPI--FPGTSQADKLVITQITTLTVSVLSASVSGLMYMPKVYIILFH 848

RESULT 11
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ID Q9QYS2 PRELIMINARY; PRT; 879 AA.
AC Q9QYS2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 3 PROTEIN.
GN GRM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=20012997; PubMed=10544282;
RA Minoshima T., Nakanishi S.;
RT "Structural organization of the mouse metabotropic glutamate receptor subtype 3 and its regulation by growth factors in cultured cortical astrocytes."
RT J. Biochem. 126:889-896(1999).
DR EMBL; AF170701; AAF06741.1; -.
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DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
```


OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yasuyuki F., Akiko J.;
RT "Structure and polymorphisms of the human metabotropic glutamate
RT receptor type 2 (hmgLur2) gene : Analysis of association with
RT schizophrenia";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045011; BAB19817.1; -
DR InterPro: IPR001828; ANF_receptor.
DR InterPro: IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 872 AA; 95567 MW; 801976D034A8100 CRC64;

Query Match 7.5%; Score 330; DB 4; Length 872;
Best Local Similarity 20.1%; Pred. No. 5.3e-17;
Matches 184; Conservative 137; Mismatches 330; Indels 264; Gaps 37;

QY 17 LLCLIASPHLQGGVAGRP-----DELHIGGIFPIAGKGGWGGQACMP----- 59
Db 4 LLALLALLLWGAVAEPAKVLTLGDLVLGLFPVHQKG--PAEDCGPVNEHRIQIR 61
QY 60 --ATRLALDDVNKPNLLPGFKLILHNSD-----QAAEVEFIS 190
Db 62 LEAMLFALDRINRPHLLPGLRGALHILSDCKDTHALEQALDFVRASLRGADSRHIC 121
QY 90 EPLGASVMYNNLLKPKMLLAG--CSTVCTTVAEAAKWNLLIVLCYGASSPALSORK 147
Db 122 PDG-----SYATHGDAPTAITGVIGGSYSDVSIQVALLRLFPQISYASTSAKLSDKS 176
QY 148 RFTFLRTHPSATVHNTRIKMKKFGWSRAIL-----QAAEVEFIS 190
Db 177 RYDFARTVPDFQAKAMAEILRFNWTYVSTVASEGDYGETGIEAFELARNICVA 236
QY 191 TVEDLENRCEAGVEIVTOSFLSDPTDAVRL--RRQDARIIVGLFVVAARRVLCEMY 248
Db 237 TSEKVGRAKRAPEGVVR-ALLQKPSARVAFLTRSEDAREL-----LAASQRL----- 285
QY 249 KQOLYGRAHVWFICWTYEDNW---YEVLKAEGITCTVEQMRIAEGHLLTEALM----- 300
Db 286 ----NASFTW----ASDGMGALESVAVGSEG-----AAEGAITIELASYPISD 326
QY 301 -----WNQNTTISGMTAEFR-----HRLNQALIEBGYDINHDPYEG 340
Db 327 FASYFQSLDPWNSRNPFREFWQRFQRCSPQRDCAAHSLRAVPFE----- 373
QY 341 YQAPLAY--DAVMSVALFNKTMERL-----TTGKSLRDFTYTQKEIADE 385
Db 374 -QESKIMEVYNAVYAMAHALNHRALCPNTRLCDAMPVNGRLYKDFVLNVKFDAPF 432
QY 386 IYAAAMSTQFLGSGVAFSPQGDRIALTQIEQIDG-----KYEKLGYY-----DTQL 434
Db 433 RPADTHNE-----VRDFRFDGIGRYNIPTYLRAAGSGRYRYQKVGYWAEGLTDLTSL 484
QY 435 DNLSQLNTEQWIGKVPQDR---TIVTHLRTVSLPLFVC--MC-----TIS 476
Db 485 --IPWASPS---AGPLPASRCEPCLQNEKVSQ--PGEVCCWCLIPCPYRYRDEFTCA 538
QY 477 SCGI-----FVAF-----ALIIFNINWKNHRR--VI 499
Db 539 DCLGLGWPNASLTGCFELPOEYIRNGDAWAVPTIACLGALATLFLVLGVFVRHNATPV 598
QY 500 QSHHPVCNTIMLFGVITCLISVILLGIDGRFVSPPEYPKIQCARAWLLSTGFTLAYGAMF 559
Db 559

Db 599 KASGRELCYILLGGVFLCYCMTFI-----FIA-KPSTAVCTLRRRLGLGTAFSVCSALL 651
QY 560 SKVVRVHRFTTKAKTPKK--VEPWKLYTMVSCLLSIDLVILLSWQIFDPLORYLETFP 617
Db 652 TKTNRARIFFGAREGAQRPRFISPAQVAICLALISGQLLIVVAVLVEAPGTGKETAP 711
QY 618 LEDPVSTDDIKIRPELEHCESSORNSMWLGLVYGFKGLILVFLGLAYETRSIKVKQIND 677
Db 712 ERREVTL-----RCNHRDASMLGSLAYNV--LLIALCTLYAFKTRKCP-ENFNE 758
QY 678 SRYVGSYIYNNVVLCLITAPVGVMIASQQDASFAFVAVIFCCFLSMLLIFVPKIVEI 737
Db 759 AKFIGTMYTTCIIWLAFLPFIVYVTTSSDYRVQVTTMCVSVSLSGSVVGLCFAPKLHIL 818
QY 738 RHPKDAESKYNPDS 752
Db 819 FQPKNVVSHRAPTS 833

RESULT 14
Q9PWEL PRELIMINARY; PRT; 977 AA.
AC Q9PWEL;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR (FRAGMENT).
GN GLUR.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Siluriformes; Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RETINA;
RA Hellmich H.L., Micci A.M., Sanchez X., Christensen B.N.;
RT "Molecular cloning, functional expression and localization of a novel
RT metabotropic glutamate receptor linked to calcium mobilization from
RT the catfish retina";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076473; AAD47893.1; -
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR001828; ANF_receptor.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
FT NON_TER 977 977
SQ SEQUENCE 977 AA; 108759 MW; BD06A67E240751CE CRC64;

Query Match 7.5%; Score 330; DB 13; Length 977;
Best Local Similarity 20.0%; Pred. No. 6.3e-17;
Matches 186; Conservative 138; Mismatches 313; Indels 292; Gaps 42;

QY 14 WIFLLC-----LIASPHLQGGVAGRPDELHIGGIFPIAGKGGWGGQAC-----M 58
Db 32 WIFCVCSPALMAHQHTPHSIKIPGDVTLGGLFPVHSGPL--GOACGBIKKEGVHRM 89
QY 59 PATRLALDDVNKPNLLPGFKL--IL-----HNSDSCEPG 92
Db 90 EAMLYALDQINSPELLPNITLGTRLDTCSDRTYALEQSLTFVQALIQKDTSDIRCSNG 149
QY 93 LGASVYNNLLYNKPKL--MLLAGCSTVCTTVAEAAKWNLLIVLCYGASSPALSDDRRFP 150
Db 150 -----EQPIIRKPERVGVIGASSVSIWAVNLRLFEIPQISYASTAPELSDNNRYD 203
QY 151 TLFRTHPSATVHNTRIKMKKFGWSRAIL-----QAAEVEFISTVEDLENRCMEAG 203
Db 203

Db 204 FFSRVPPDSYQOAMVDIVKALGNHYVFIILASEGNYGESGVDAFVQISREAGGICIAQS 263
QY 204 VEIVTOSFLSDPT-----DAV--RNLRRQDARIIVGLFYVVAARRVLCMEYKQOOLYGRAH 257
Db 264 MKIP-----RDPKPGEPDKIIKRLMTPNARGIIFANEDDIKQVLEAARRANLTGH-- 315
QY 258 VWFIQWYEDNW-----YEVNKAEGITCTVEQMRNAAEG---HLTTEALMWNON 304
Db 316 -FKVVG--SDSWGAKSAPILDNEEV---AEG-AVTPILPKRASVEGFDQYFTSRSL---EN 365
QY 305 NOTTI--SGMTAEFRHRLNALIB-----EGYD-INHDYRPEGYOEAPLAYDAVWS 353
Db 366 NRRNIWAEFWEDDERCKLTPGKIDPEKKCTKERIGRDSPEQBKGVOFVDAVYA 425
QY 354 VALAFNKTMRLETTGKSLRDLFTYTDKEIADIEYAAAMSTQFLVSGV--VAFSSQGDRIA 412
Db 426 MAHALHNHQTCAARGTGLCKMDPVEGRLLLSYIRAVN---FNGSAGTGVLFNENGD--- 479
QY 413 LTOIEQMDIGYKELGYDITOLDNLS-----WJNT--- 442
Db 480 -----APGRYDIFQY---QFSNTSPGYKVIGQSFISSAKTSPGYKVFQOWTNILG 529
QY 443 -----EOWIGGK----- 449
Db 530 INEVEEMQWQSGEHYIPASVCSFPCQGERKKMWKGVPCCHCEPCDQGYQYQVGLTCEM 589
QY 450 VPQD-RTIVTHVLRVTS-----LPLFVCMCTISSCGIFVAFALIIFNINWKKH 495
Db 590 CPFDMPRTANHTACTPTPIIKLDWHSWAVVPMFLAI-----LGIAATLSVVIVFREND 644
QY 496 RVVIOSSHPVNTIMLFGV-IICILSVILLGIDGRFVSPEEPKICOARAWLLSTGFTLA 554
Db 645 TPIVRASGRELSYLLTGIFLIYITFLMIA-----EPNTVVCALRLLGLGMCIT 696
QY 555 YGAMFSKVMVRHRETTAK---TDPKKVPEPKLYTMVSGLLSIDLVILLWQIFDPLQR 611
Db 697 YSAMLTKNRIYRPEQKKSWAP-KFISPTSQLVIFILVFSQVIGVFIW----- 747
QY 612 YLETFPLEDDPVSTDDIKIR---PELEH---CESORNSMWLGLVYGFKGLILVFLGLFLA 664
Db 748 ---FGVPPHTIVDYDELPPNPPELARGILKCDMSDLSLICLSYSI--LLMVTCTVYA 801
QY 665 YETRSIKVKQINDSYGMSIYNVVLCLITAPV--GMVIAQQODASFAFVALAIFCCF 722
Db 802 VKSRGVP-ETFEAKPIGFTYTTTCIVWLAFVPIFFGTAQSHGEDV----- 846
QY 723 LSMILLIFVPKVIEWIRHPKDKAESYNDP 751
Db 847 -----HPDDHADRVHEPE 859

RESULT 15
Q98UC5
ID Q98UC5 PRELIMINARY; PRT: 1188 AA.
AC Q98UC5;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 5 SPLICED VARIANT B.
GN MGLUR5B.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Storchmann L.L., Stormann T.M., Parks T.N.;
RT "Molecular Cloning and Functional Expression of Chick Metabotropic
RT Glutamate Receptor 5 Splice Variants";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF227202; AAK01487.1; -

KW Receptor.
SQ SEQUENCE 1188 AA; 132053 MW; 6C179BF8C8045BBD CRC64;
Query Match 6.8%; Score 299.5; DB 13; Length 1188;
Best Local Similarity 20.1%; Pred. No. 2.1e-14;
Matches 202; Conservative 153; Mismatches 395; Indels 253; Gaps 40;
QY 16 FLCLIASPHLOGGVAGRPDELHIGGIFPI-----AGKGGWGGQACMPATR 62
Db 20 FGLVSAQANERRVVAHMPGDIIGALFVHHQPTVDKVERKCGVEQYGIQVREAML 79
QY 63 LALDDVKNQNPILPGFKLILHSND-----SECEPGL-----GA 95
Db 80 HTLDRLNLDPTLNPITLGCIEIRDSCHWSAVALAQSTIEFIRDSLISSEEGVMVRCVDS 139
QY 96 SVMYNLLYNKPKQLMLLAGCSTVCTTVAEAKMNNLIVLCYGASSPALSDDKRPETLFT 155
Db 140 SSSFH--SKAPIGVIGPGSSVAIQVONLLQFLNIPQIAYSATSMDSKTLFKYFMRV 197
QY 156 HPSATVHNPTRIKMKFGMSRVAILQQAEEVFISTVEDLENRCMEAGVEIVTRQSFSD 215
Db 198 VPSDAQARAMVDIVKRYNNTYVSATVTEGNYGESGMEAFKMAAKGEGICIAHSYKIYSN 257
QY 216 PTD-----AVNLRQ--DARIIVGLFYVVAARRVLCMEYKQOOLYGRAHVVFFIGWYEDN 268
Db 258 AGEQSFDKLLRKLRLSHLPKARVACFCGEMTVRGLLMAMRRRLGLAGE-----FLLGSDG 312
QY 269 WYEVNKAEGITCTVEQMRNAAEG---HLTTEALMWNONQTTISGMT-----ABEFR 318
Db 313 W-----ADRYDVTGYOREAVGGITKLQSPDVKWFDDYLELRPETNHRNPNFQEFWQ 366
QY 319 HRLNQAALIEBYDINHRY-----PEGYQEAFLAY--DAVWSVALAFNKTMRER 365
Db 367 HRFQCL--EGFQENPKYKNTCTSMTRTQHVQDSKMGFVINAIYSMAVGLHNMQLSL 424
QY 366 TTGKSLRDTYTDKEI-ADEIYAAMNSTOFLVSG--VAFSSQGDRIALTOIEQMDIGK 423
Db 425 CPGVVGLCD---AMKPIDGRKLLLESMTNFTGVSGDMILFDENGDS-----PGR 471
QY 424 YELGYVYDTQDLNLSWLNTEQWIGGKVPQDRTIV---THVLRV-SLPL----- 468
Db 472 YEIMNFKKMGKDFDYINVSWDNGELKMDDEIWESEKNNIIRSVCEPCKEQIKVIRK 531
QY 469 -----FVC-MCTISS-----CGIF-----VA 483
Db 532 GEVSCCWTCTCKENEYVFEYTCCKACQLGSPWDELTCGLIPVQVLRWGDPEPIAAV 591
QY 484 FALI-----IFNWKHRRVIOSSHPCVNTIMLFGVII-----CLISVILLGID 527
Db 592 FACIGLLATLFTVTAIFTMYRDTVPVKSRRSLC-YIILAGICLGLYCTFCLIA----- 643
QY 528 GRFVSPEEYKICOARAWLLSTGFTLAYGAMFSKVMVRHRETTAKTDPKKKVPKWLKT 587
Db 644 ----KPOOI--CYQLQIGIGLSPAMSYSAVLTNTNRIARILAGS-----KKKCTKKPRF 693
QY 588 MVSGLLSIDLVILLSWQIFDPLQRYLETFFLEDPVSTDDIKIRPELEHCEQSQRNSMWLG 647
Db 694 MSACQALVIAFILICIQ---LGIIVAFIMEPPDIMHDYPSIREVYLIC---NTNLG 745
QY 648 LV--YGFKGLILVFLGFLAYETRSIKVKQINDSYGMSIYNVVLCLITAPVGMVIAQ 705
Db 746 VVTPGLYNGLLILSCTFTVAFKRNVA-NFNEAKYIAFTMYTTCIIWLAFVPI----- 797
QY 706 QDASFVAFVALAIFCCF-----LSMLLIFVPKVIEWIRHPKDKAESKYNPDSAI----- 754
Db 798 ----YFGSNYKIIITMCFVSLSATVLCGMFVPKVYIILAKPERNVRSAFTTSTVVRMHV 853
QY 755 ----SKEDERYQKLV-----TENQOL-----ORLTQKEKIRVLRQRLVERGDAKGT 799
Db 854 GDGKSSAAARSSSLVNLWKRKRGSGETLYKGRRLAPHKSE-----IECTPKGS 904
QY 800 ELNG--ATGVASAAVATTSTQPASLINSSAHATPAATLAIQGE 840

Db 905 MNGGRATWTSSNGKSVSWAQNEKSSRGHLWQRLSIHINKKE 947

Search completed: April 30, 2002, 10:16:30
Job time: 237 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:13:08 ; Search time 14.82 Seconds

(without alignments)

2078.168 Million cell updates/sec

Title: US-09-715-962-2

Perfect score: 4374

Sequence: 1 MRKDMFSDGAVTFWIFLLCL.....LINSSAHATPAATLAIQTQE 840

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2031.5	46.4	960	1 GBR1_MOUSE	O9wv18 mus musculus
2	2030.5	46.4	961	1 GBR1_HUMAN	O9ubs5 homo sapien
3	2004	45.8	991	1 GBR1_RAT	O920u4 rattus norv
4	1290	29.5	941	1 GBR2_HUMAN	O75899 homo sapien
5	1286	29.4	940	1 GBR2_RAT	O88871 rattus norv
6	366.5	8.4	976	1 MGR_DROME	P91685 drosophila
7	361	8.3	908	1 MGR8_RAT	P70579 rattus norv
8	360	8.2	908	1 MGR8_HUMAN	O00222 homo sapien
9	356.5	8.2	912	1 MGR4_RAT	P31423 rattus norv
10	355	8.1	908	1 MGR8_MOUSE	P47743 mus musculus
11	355	8.1	915	1 MGR7_HUMAN	O14831 homo sapien
12	353	8.1	912	1 MGR4_HUMAN	O14833 homo sapien
13	353	8.1	915	1 MGR7_RAT	P35400 rattus norv
14	334.5	7.6	871	1 MGR6_RAT	P35349 rattus norv
15	333	7.6	879	1 MGR3_RAT	P31422 rattus norv
16	323	7.4	877	1 MGR3_HUMAN	O14832 homo sapien
17	322	7.4	872	1 MGR2_HUMAN	O14416 homo sapien
18	318	7.3	872	1 MGR2_RAT	P31421 rattus norv
19	313.5	7.2	877	1 MGR6_HUMAN	O15303 homo sapien
20	305	7.0	1203	1 MGR5_RAT	P31424 rattus norv
21	297.5	6.8	1212	1 MGR5_HUMAN	P41594 homo sapien
22	294	6.7	999	1 MGR1_CAEEL	O09630 caenorhabdi
23	276	6.3	1194	1 MGR1_HUMAN	O13255 homo sapien
24	268	6.1	1199	1 MGR1_RAT	P23385 rattus norv
25	227.5	5.2	1079	1 CASR_MOUSE	O9qy96 mus musculus
26	219.5	5.0	1078	1 CASR_HUMAN	P41180 homo sapien
27	212.5	4.9	1079	1 CASR_RAT	P48442 rattus norv
28	198.5	4.5	1085	1 CASR_BOVIN	P35384 bos taurus
29	184.5	4.2	1047	1 ANPB_RAT	P16067 rattus norv
30	181.5	4.1	1047	1 ANPB_BOVIN	P46197 bos taurus
31	177.5	4.1	1047	1 ANPB_HUMAN	P20594 homo sapien
32	172	3.9	1050	1 ANPB_ANGJA	P55202 anguilla ja
33	159	3.6	540	1 ANPC_HUMAN	P17342 homo sapien

34	156	3.6	1061	1 ANPC_HUMAN	P16066 homo sapien
35	154	3.5	535	1 ANPC_RAT	P41740 rattus norv
36	147.5	3.4	1057	1 ANPC_MOUSE	P18910 rattus norv
37	146	3.3	1057	1 CYGL_MOUSE	P18293 mus musculus
38	145	3.3	1137	1 CYGL_CAEEL	Q09435 caenorhabdi
39	144.5	3.3	536	1 ANPC_MOUSE	P70180 mus musculus
40	142	3.2	537	1 ANPC_BOVIN	P10730 bos taurus
41	137.5	3.1	836	1 GLK1_MOUSE	Q60934 mus musculus
42	137.5	3.1	1103	1 CYGF_BOVIN	O02740 bos taurus
43	132.5	3.0	1108	1 CYGF_HUMAN	P51841 homo sapien
44	128	2.9	918	1 GLK1_HUMAN	P39086 homo sapien
45	128	2.9	1110	1 CYGX_RAT	P51839 rattus norv

ALIGNMENTS

RESULT 1	
GBR1_MOUSE	
ID	GBR1_MOUSE STANDARD; PRT; 960 AA.
AC	Q9WV18; Q9WV15; Q9WV16; Q9WV17; Q9WU48;
DT	20-AUG-2001 (Rel. 40, Created)
DT	20-AUG-2001 (Rel. 40, Last sequence update)
DT	20-AUG-2001 (Rel. 40, Last annotation update)
DE	GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1 PRECURSOR (GABA-B RECEPTOR 1) (GABA-B-R1) (GB1).
DE	GABBR1.
GN	Mus musculus (Mouse).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A. (ISOFORM 1A).
RX	MEDLINE-20237752; PubMed-10773016;
RA	Sullivan R., Chateaufneuf A., Coulombe N., Kolakowski L.F. Jr., Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K., Abramovitz M., O'Neill G.P., Ng G.Y.K.;
RT	"Coexpression of full-length gamma-aminobutyric acid(B) (GABA(B)) receptors with truncated receptors and metabotropic glutamate receptor 4 supports the GABA(B) heterodimer as the functional receptor.";
RT	J. Pharmacol. Exp. Ther. 293:460-467(2000).
RN	[2]
RP	SEQUENCE FROM N.A. (ISOFORMS 1B; 1C AND 1D).
RA	Younger R.;
RT	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A. (ISOFORM 1B).
RA	Lamp K., Humeny A., Nikolic Z., Becker C.-M.;
RT	"Cloning of the murine GABABR1b receptor.";
RT	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN	[4]
RP	SEQUENCE FROM N.A. (ISOFORM 1A).
RA	Humeny A., Lamp K., Nikolic Z., Becker C.-M.;
RT	"Mouse GABA-B receptor cDNA sequence.";
RT	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN	[5]
RP	RIA-P2 INTERACTION.
RA	MEDLINE-99102694; PubMed-9872744;
RA	Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A., Kornau H.-C.;
RT	"Role of heteromer formation in GABAB receptor function.";
RT	Science 283:74-77(1999).
CC	-I- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G-PROTEINS THAT INHIBITS ADENYL CYCLASE ACTIVITY, STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS, INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE

[illegible][illegible]

Query Match	46.4%;	Score 2031.5;	DB 1;	Length 960;
Best Local Similarity	49.4%;	Pred. No. 7.4e-148;		
Matches 385;	Conservative 150;	Mismatches 221;	Indels 23;	Gaps 8;

[illegible]

Qy 499 IQSSHPVNTIMLFGVVICLLSVILLGIDGRFVSPEEYKICQARAWLLSTGETLAYGAM 558
Db 621 IONSQPNLNLTAFCGSLAALAVFLGLDGYHIGRSQFPFVCOARLWLGLGFSGLYGS 680
Qy 559 FSKVNRVHRFTTK--AKTDPKKVPEPKLYTMVSGLLSIDLVLLSWQIFDPLQRYLET 616
Db 681 FTKIWWHTVFTKKEKEMRTLEPKLYATVGLLVGMDILTAIWOIVDPLHRTIET 740
Qy 617 PLEDVSTDDIKIRPELHESQSRNSMGLVYGFGLVFLGFLAYETRSIKYKQIN 676
Db 741 AKPEKEDI-DVSIPLQLEHCSKKMTWLGIFYGYKGLLLGIFLAYETKSVSTEKIN 799
Qy 677 DSRVYGMIIYVVLCLITAPVGMVIAOQDASFALVALAVIFCCFLSMLLIFVPKVIEW 736
Db 800 DHRVGMAYINAVVLCITAPVMTLSQDAAFAFASIAIVSSYITIVLFLVPKMRRL 859
Qy 737 IRHP--KKAESKYNPDSAIKDEDEYOKLYTENEOLQRLJTOKEKIRVLRORLVER 793
Db 860 ITRGEQSEADTKMTGSGSTNNNEEKSRLLEKENRELEKITAEEKRVSLELHQLOS 918
RESULT 2
GBR1_HUMAN
ID GBR1_HUMAN STANDARD; PRT; 961 AA.
AC Q9UBS5; G95375; Q9UQ00; O96022; O95975; O95468;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GAMMA-AMINOBTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1 PRECURSOR (GABA-B
RECEPTOR 1) (GABA-B-R1) (GB1).
GN GABBR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
RC TISSUE=Cerebellum;
RX Kaufmann K., Schuler V., Mosbacher J., Bischoff S., Bittiger H.,
Held J., Froestl W., Leonhard S., Pfaff T., Karschin A., Bettler B.;
"Human gamma-aminobutyric acid type B receptors are differentially
expressed and regulate inwardly rectifying K⁺ channels.";
Proc. Natl. Acad. Sci. U.S.A. 95:14991-14996(1998).
[2]
RN SEQUENCE FROM N.A. (ISOFORMS 1A; 1B AND 1C).
RC TISSUE=Cerebellum;
RX MEDLINE=99087321; PubMed=9872316;
RA White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H.,
Barnes A.A., Emson P., Foord S.M., Marshall F.H.;
"Heterodimerization is required for the formation of a functional
GABA(B) receptor.";
Nature 396:679-682(1998).
[3]
RN SEQUENCE FROM N.A. (ISOFORM 1A).
RC TISSUE=Brain;
RA Stropp U., Raming K.;
"Human mRNA for GABA-B1a receptor.";
Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A. (ISOFORM 1A).
RC TISSUE=Fetal brain;
RX MEDLINE=98440782; PubMed=9753614;
RA Grifa A., Totaro A., Rommens J.M., Carella M., Roetto A., Borgato L.,
Zelante L., Gasparini P.;
"GABA (gamma-aminobutyric acid) neurotransmission: identification and
fine mapping of the human GABAB receptor gene.";
Biochem. Biophys. Res. Commun. 250:240-245(1998).
[5]
RN SEQUENCE FROM N.A. (ISOFORM 1A).
RX MEDLINE=99014802; PubMed=9798068;
RA Gosi V.L., Choi J., Ahn J., Bowlus C.L., Raha-Chowdhury R.,

RA Gruen J.R.;
"Human gamma-aminobutyric acid B receptor gene: complementary DNA
cloning, expression, chromosomal location, and genomic organization.";
Biol. Psychiatry 44:659-666(1998).
[6]
RN SEQUENCE FROM N.A. (ISOFORM 1C).
RC TISSUE=Cerebellum;
RA Fraser N.J.;
Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
[7]
RN SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B), AND VARIANTS V-20 AND S-489.
RC TISSUE=Fetal brain;
RX MEDLINE=20184290; PubMed=9933300;
RA Peters H.C., Kaemmer G., Volz A., Kaupmann K., Ziegler A., Bettler B.,
Epplen J.T., Sander T., Riess O.;
"Mapping, genomic structure, and polymorphisms of the human GABAB1
receptor gene: evaluation of its involvement in idiopathic
generalized epilepsy.";
Neurogenetics 2:47-54(1998).
[8]
RN SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
RA Younger R.;
Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
[9]
RN SEQUENCE FROM N.A. (ISOFORM 1A).
RC TISSUE=Cerebellum;
RX MEDLINE=99108069; PubMed=9889352;
RA Makoff A.;
"Molecular cloning of human GABAB1 and its tissue distribution.";
Brain Res. Mol. Brain Res. 64:137-140(1999).
[10]
RN SEQUENCE FROM N.A. (ISOFORM 1E).
RC TISSUE=Prostate;
RX MEDLINE=20493604; PubMed=10906333;
RA Schwarz D.A., Barry G., Eliasof S.D., Petroski R.E., Conlon P.J.,
Maki R.A.;
"Characterization of gamma-aminobutyric acid receptor GABAB(1e), a
GABAB(1) splice variant encoding a truncated receptor.";
J. Biol. Chem. 275:32174-32181(2000).
[11]
RN VARIANTS VAL-20 AND SER-489.
RX MEDLINE=99332183; PubMed=10402495;
RA Sander T., Peters C., Kaemmer G., Samochowiec J., Zirra M.,
Mischke D., Ziegler A., Kaupmann K., Bettler B., Epplen J.T.,
Riess O.;
"Association analysis of exonic variants of the gene encoding the
GABAB receptor and idiopathic generalized epilepsy.";
Am. J. Med. Genet. 88:305-310(1999).
[12]
RN R1A-R2 INTERACTION.
RX MEDLINE=20337752; PubMed=10773016;
RA Sullivan R., Chateauf A., Coulombe N., Kolakowski L.F. Jr.,
Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K.,
Abramovitz M., O'Neill G.P., Ng G.Y.K.;
"Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B))
receptors with truncated receptors and metabotropic glutamate
receptor 4 supports the GABA(B) heterodimer as the functional
receptor.";
J. Pharmacol. Exp. Ther. 293:460-467(2000).
[13]
RN R1A-R2 INTERACTION.
RX MEDLINE=99102694; PubMed=9872744;
RA Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
Kornau H.-C.;
"Role of heteromer formation in GABAB receptor function.";
Science 283:74-77(1999).
CC -1- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES
INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING

CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
 CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
 CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
 CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
 CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
 CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
 CC ANTINOCEPTION. ACTIVATED BY (-)-BACLOFEN, CGP27492 AND BLOCKED
 CC BY PHACLOFEN.
 CC
 CC -!- FUNCTION: ISOFORM 1E FUNCTION MAY BE TO REGULATE THE AVAILABILITY
 CC OF FUNCTIONAL GABA-B-RIA/GABA-B-R2 HETERODIMERS BY COMPETING FOR
 CC GABA-B-R2 DIMERIZATION. THIS COULD EXPLAIN THE OBSERVATION THAT
 CC CERTAIN SMALL MOLECULE LIGANDS EXHIBIT DIFFERENTIAL AFFINITY FOR
 CC CENTRAL VERSUS PERIPHERAL SITES.
 CC
 CC -!- COFACTOR: REQUIRES CALCIUM FOR HIGH AFFINITY BINDING TO GABA.
 CC
 CC -!- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
 CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
 CC HAPPEN. ISOFORM 1E (WITHOUT C-TERMINAL INTRACELLULAR DOMAIN) IS
 CC UNABLE TO DIMERIZE VIA A COILED-COIL INTERACTION WITH GABA-B-R2.
 CC
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
 CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
 CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
 CC PLASMA MEMBRANE. ISOFORM 1E CAN ALSO BE SECRETED.
 CC
 CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS: 1A (SHOWN HERE), 1B, 1C, 1D AND
 CC 1E/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORMS
 CC CORRESPONDING TO THE FULL RECEPTOR ARE ESSENTIALLY FOUND IN THE
 CC CENTRAL NERVOUS SYSTEM (CNS). ISOFORM 1E IS THE MAJOR ISOFORM IN
 CC ALMOST ALL PERIPHERAL TISSUES. IT MAY ACT AS AN ANTAGONIST OF
 CC GABA-B RECEPTORS, BEING ABLE TO DISRUPT THE NORMAL ASSOCIATION
 CC BETWEEN ISOFORM 1A AND GABA-B-R2.
 CC
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN AND WEAKLY IN HEART,
 CC SMALL INTESTINE AND UTERUS. MOSTLY EXPRESSED IN GRANULAR CELL AND
 CC MOLECULAR LAYER FOR ISOFORM 1A AND IN PURKINJE CELLS FORM ISOFORM
 CC 1B. ISOFORM 1E IS PREDOMINANTLY EXPRESSED IN PERIPHERAL TISSUES AS
 CC KIDNEY, LUNG, TRACHEA, COLON, SMALL INTESTINE, STOMACH, BONE
 CC MARROW, THYMUS AND MAMMARY GLAND.
 CC
 CC -!- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
 CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 2. THE
 CC LINKER REGION BETWEEN THE TRANSMEMBRANE DOMAIN 3 (TM 3) AND THE
 CC TRANSMEMBRANE DOMAIN 4 (TM 4) PROBABLY PLAY A ROLE IN THE
 CC SPECIFICITY FOR G-PROTEIN COUPLING.
 CC
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC
 CC -!- GABA-B RECEPTOR SUBFAMILY.
 CC
 CC -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
 CC
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 CC DR EMBL; AJ225283; CAA12614.1; -
 CC DR EMBL; AJ225284; CAA12615.1; -
 CC DR EMBL; AJ225285; CAA12616.1; -
 CC DR EMBL; AJ225286; CAA12617.1; -
 CC DR EMBL; AJ225287; CAA12618.1; -
 CC DR EMBL; AJ225288; CAA12619.1; -
 CC DR EMBL; AJ225289; CAA12620.1; -
 CC DR EMBL; AJ225290; CAA12621.1; -
 CC DR EMBL; AJ225291; CAA12622.1; -
 CC DR EMBL; AJ225292; CAA12623.1; -
 CC DR EMBL; AJ225293; CAA12624.1; -
 CC DR EMBL; AJ225294; CAA12625.1; -
 CC DR EMBL; AJ225295; CAA12626.1; -
 CC DR EMBL; AJ225296; CAA12627.1; -
 CC DR EMBL; AJ225297; CAA12628.1; -
 CC DR EMBL; AJ225298; CAA12629.1; -
 CC DR EMBL; AJ225299; CAA12630.1; -
 CC DR EMBL; AJ225300; CAA12631.1; -
 CC DR EMBL; AJ225301; CAA12632.1; -
 CC DR EMBL; AJ225302; CAA12633.1; -
 CC DR EMBL; AJ225303; CAA12634.1; -
 CC DR EMBL; AJ225304; CAA12635.1; -
 CC DR EMBL; AJ225305; CAA12636.1; -
 CC DR EMBL; AJ225306; CAA12637.1; -
 CC DR EMBL; AJ225307; CAA12638.1; -
 CC DR EMBL; AJ225308; CAA12639.1; -
 CC DR EMBL; AJ225309; CAA12640.1; -
 CC DR EMBL; AJ225310; CAA12641.1; -
 CC DR EMBL; AJ225311; CAA12642.1; -
 CC DR EMBL; AJ225312; CAA12643.1; -
 CC DR EMBL; AJ225313; CAA12644.1; -
 CC DR EMBL; AJ225314; CAA12645.1; -
 CC DR EMBL; AJ225315; CAA12646.1; -
 CC DR EMBL; AJ225316; CAA12647.1; -
 CC DR EMBL; AJ225317; CAA12648.1; -
 CC DR EMBL; AJ225318; CAA12649.1; -
 CC DR EMBL; AJ225319; CAA12650.1; -
 CC DR EMBL; AJ225320; CAA12651.1; -
 CC DR EMBL; AJ225321; CAA12652.1; -
 CC DR EMBL; AJ225322; CAA12653.1; -
 CC DR EMBL; AJ225323; CAA12654.1; -
 CC DR EMBL; AJ225324; CAA12655.1; -
 CC DR EMBL; AJ225325; CAA12656.1; -
 CC DR EMBL; AJ225326; CAA12657.1; -
 CC DR EMBL; AJ225327; CAA12658.1; -
 CC DR EMBL; AJ225328; CAA12659.1; -
 CC DR EMBL; AJ225329; CAA12660.1; -
 CC DR EMBL; AJ225330; CAA12661.1; -
 CC DR EMBL; AJ225331; CAA12662.1; -
 CC DR EMBL; AJ225332; CAA12663.1; -
 CC DR EMBL; AJ225333; CAA12664.1; -
 CC DR EMBL; AJ225334; CAA12665.1; -
 CC DR EMBL; AJ225335; CAA12666.1; -
 CC DR EMBL; AJ225336; CAA12667.1; -
 CC DR EMBL; AJ225337; CAA12668.1; -
 CC DR EMBL; AJ225338; CAA12669.1; -
 CC DR EMBL; AJ225339; CAA12670.1; -
 CC DR EMBL; AJ225340; CAA12671.1; -
 CC DR EMBL; AJ225341; CAA12672.1; -
 CC DR EMBL; AJ225342; CAA12673.1; -
 CC DR EMBL; AJ225343; CAA12674.1; -
 CC DR EMBL; AJ225344; CAA12675.1; -
 CC DR EMBL; AJ225345; CAA12676.1; -
 CC DR EMBL; AJ225346; CAA12677.1; -
 CC DR EMBL; AJ225347; CAA12678.1; -
 CC DR EMBL; AJ225348; CAA12679.1; -
 CC DR EMBL; AJ225349; CAA12680.1; -
 CC DR EMBL; AJ225350; CAA12681.1; -
 CC DR EMBL; AJ225351; CAA12682.1; -
 CC DR EMBL; AJ225352; CAA12683.1; -
 CC DR EMBL; AJ225353; CAA12684.1; -
 CC DR EMBL; AJ225354; CAA12685.1; -
 CC DR EMBL; AJ225355; CAA12686.1; -
 CC DR EMBL; AJ225356; CAA12687.1; -
 CC DR EMBL; AJ225357; CAA12688.1; -
 CC DR EMBL; AJ225358; CAA12689.1; -
 CC DR EMBL; AJ225359; CAA12690.1; -
 CC DR EMBL; AJ225360; CAA12691.1; -
 CC DR EMBL; AJ225361; CAA12692.1; -
 CC DR EMBL; AJ225362; CAA12693.1; -
 CC DR EMBL; AJ225363; CAA12694.1; -
 CC DR EMBL; AJ225364; CAA12695.1; -
 CC DR EMBL; AJ225365; CAA12696.1; -
 CC DR EMBL; AJ225366; CAA12697.1; -
 CC DR EMBL; AJ225367; CAA12698.1; -
 CC DR EMBL; AJ225368; CAA12699.1; -
 CC DR EMBL; AJ225369; CAA12700.1; -
 CC DR EMBL; AJ225370; CAA12701.1; -
 CC DR EMBL; AJ225371; CAA12702.1; -
 CC DR EMBL; AJ225372; CAA12703.1; -
 CC DR EMBL; AJ225373; CAA12704.1; -
 CC DR EMBL; AJ225374; CAA12705.1; -
 CC DR EMBL; AJ225375; CAA12706.1; -
 CC DR EMBL; AJ225376; CAA12707.1; -
 CC DR EMBL; AJ225377; CAA12708.1; -
 CC DR EMBL; AJ225378; CAA12709.1; -
 CC DR EMBL; AJ225379; CAA12710.1; -
 CC DR EMBL; AJ225380; CAA12711.1; -
 CC DR EMBL; AJ225381; CAA12712.1; -
 CC DR EMBL; AJ225382; CAA12713.1; -
 CC DR EMBL; AJ225383; CAA12714.1; -
 CC DR EMBL; AJ225384; CAA12715.1; -
 CC DR EMBL; AJ225385; CAA12716.1; -
 CC DR EMBL; AJ225386; CAA12717.1; -
 CC DR EMBL; AJ225387; CAA12718.1; -
 CC DR EMBL; AJ225388; CAA12719.1; -
 CC DR EMBL; AJ225389; CAA12720.1; -
 CC DR EMBL; AJ225390; CAA12721.1; -
 CC DR EMBL; AJ225391

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
 RC STRAIN=RICO; TISSUE=Brain cortex, and Cerebellum;
 RX MEDLINE=97222131; PubMed=9069281;
 RA Kaupmann K., Hugel K., Heid J., Flor P.J., Bischoff S., Michel S.J.,
 RA McMaster C., Angst C., Bittiger H., Froestl W., Bettler B.;
 RT "Expression cloning of GABA(B) receptors uncovers similarity to
 RT metabotropic glutamate receptors.";
 RL Nature 386:239-246(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1C AND 1D).
 RC TISSUE=Cerebellum;
 RX MEDLINE=99092370; PubMed=9875211;
 RA Isomoto S., Kaibara M., Sakurai-Yamashita Y., Nagayama Y., Uezono Y.,
 RA Yano K., Taniyama K.;
 RT "Cloning and tissue distribution of novel splice variants of the rat
 RT GABAB receptor.";
 RL Biochem. Biophys. Res. Commun. 253:10-15(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1E).
 RC STRAIN=Wistar; TISSUE=Hippocampus;
 RX MEDLINE=99388283; PubMed=10457184;
 RA Praff T., Malitschek B., Kaupmann K., Prezeau L., Pin J.-P.,
 RA Bettler B., Karschin A.;
 RT "Alternative splicing generates a novel isoform of the rat
 RT metabotropic GABA(B)R1 receptor.";
 RL Eur. J. Neurosci. 11:2874-2882(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1A), AND R1A-R2 INTERACTION.
 RC TISSUE=Brain;
 RX MEDLINE=99175124; PubMed=10075644;
 RA Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan R.,
 RA Kargman S., Chateaufort A., Tsukamoto N., McDonald T., Whiting P.,
 RA Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
 RA Bonner T.I., O'Neill G.P.;
 RT "Identification of a GABAB receptor subunit, gb2, required for
 RT functional GABAB receptor activity.";
 RL J. Biol. Chem. 274:7607-7610(1999).
 RN [5]
 RP TISSUE DISTRIBUTION.
 RX MEDLINE=20121644; PubMed=10658574;
 RA Belley M., Sullivan R., Reeves A., Evans J.F., O'Neill G.P.,
 RA Ng G.Y.K.;
 RT "Synthesis of the nanomolar photoaffinity GABA(B) receptor ligand CGP
 RT 71872 reveals diversity in the tissue distribution of GABA(B) receptor
 RT forms.";
 RL Bioorg. Med. Chem. 7:2697-2704(1999).
 RN [6]
 RP R1A-R2 INTERACTION.
 RX MEDLINE=99102694; PubMed=9872744;
 RA Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
 RA Kornau H.-C.;
 RT "Role of Heteromer Formation in GABA-B Receptor Function.";
 RL Science 283:74-77(1999).
 RN [7]
 RP MUTAGENESIS OF SER-247; SER-268 AND SER-269.
 RX MEDLINE=20159055; PubMed=10692480;
 RA Galvez T., Urwyler S., Prezeau L., Mosbacher J., Joly C.,
 RA Malitschek B., Heid J., Brabet I., Froestl W., Bettler B.,
 RA Kaupmann K., Pin J.-P.;
 RT "Ca(2+) requirement for high-affinity gamma-aminobutyric acid (GABA)
 RT binding at GABA(B) receptors: involvement of serine 269 of the
 RT GABA(B)R1 subunit.";
 RL Mol. Pharmacol. 57:419-426(2000).
 RL [8]
 CC -1- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
 CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
 CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM CHANNELS AND MODULATES
 CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
 CC

CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
 CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
 CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
 CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
 CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
 CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
 CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
 CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
 CC ANTINOCICEPTION.
 CC -1- COFACTOR: REQUIRES CALCIUM FOR HIGH AFFINITY BINDING TO GABA.
 CC -1- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
 CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
 CC HAPPEN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
 CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
 CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
 CC PLASMA MEMBRANE.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: 1A, 1B, 1C, 1D AND 1E (SHOWN
 CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ISOFORMS 1A, 1B AND 1C ARE EXPRESSED IN
 CC TESTIS, STOMACH, SPINAL CORD AND BRAIN INCLUDING CEREBRAL CORTICAL
 CC LAYERS, PYRAMIDAL CELL LAYERS OF THE HIPPOCAMPUS, GRANULAR CELL
 CC LAYERS OF THE DENTATE GYRUS, BASAL GANGLIA, CEREBELLUM
 CC (PREDOMINANTLY IN PURKINJE CELLS FOLLOWED BY GRANULAR LAYER).
 CC ISOFORM 1B IS ALSO EXPRESSED IN KIDNEY AND LIVER. ISOFORM 1D IS
 CC EXPRESSED IN FOREBRAIN, CEREBELLUM, EYE, KIDNEY, AND URINARY
 CC BLADDER.
 CC -1- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
 CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 2. THE
 CC LINKER REGION BETWEEN THE TRANSMEMBRANE DOMAIN 3 (TM 3) AND THE
 CC TRANSMEMBRANE DOMAIN 4 (TM 4) PROBABLY PLAY A ROLE IN THE
 CC SPECIFICITY FOR G-PROTEIN COUPLING.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC GABA-B RECEPTOR SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
 CC -1- CAUTION: ISOFORM 1E HAS BEEN CALLED 1C IN REF.3.
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 CC -----
 CC EMBL: Y10369; CAA71398.1; -;
 CC EMBL: Y10370; CAA71399.1; -;
 CC EMBL: AB016160; BAA34708.1; -;
 CC EMBL: AB016161; BAA34709.1; -;
 CC EMBL: AF110797; AAD19656.1; -;
 CC EMBL: AF110796; AAD19656.1; JOINED.
 CC EMBL: AF110797; AAD19657.1; -;
 CC EMBL: AF110796; AAD19657.1; JOINED.
 CC EMBL: AF110797; AAD19658.1; -;
 CC EMBL: AF110796; AAD19658.1; JOINED.
 CC EMBL: AF110797; AAD19659.1; -;
 CC EMBL: AF110796; AAD19659.1; JOINED.
 CC HSSP: P10998; 1VVC.
 CC InterPro: IPR001828; ANF_receptor.
 CC InterPro: IPR000337; GPCR_Mgr.
 CC InterPro: IPR000436; Sushi_SCR_OCP.
 CC Pfam: PF00003; 7tm_3; 1.
 CC Pfam: PF01094; ANF_receptor; 1.
 CC Pfam: PF00084; sushi; 2.
 CC PRINTS: PR01176; GABABRECEPTR.
 CC PRINTS: PR01177; GABABRECEPTR.
 CC SMART: SM00032; CCP; 2.
 CC PROSITE: PS000979; G_PROTEIN_RECEP_F3_1; FALSE_NEG.
 CC PROSITE: PS000980; G_PROTEIN_RECEP_F3_2; FALSE_NEG.
 CC PROSITE: PS000981; G_PROTEIN_RECEP_F3_3; FALSE_NEG.
 CC PROSITE: PS00259; G_PROTEIN_RECEP_F3_4; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 CC Postsynaptic membrane; Coiled coil; Repeat; Alternative splicing.
 KW

FT	SIGNAL	1	16	POTENTIAL.	
FT	CHAIN	17	991	GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1.	
FT	DOMAIN	17	590	EXTRACELLULAR (POTENTIAL).	
FT	TRANSFEM	591	611	I (POTENTIAL).	
FT	DOMAIN	612	630	CYTOLASMIC (POTENTIAL).	
FT	TRANSFEM	631	651	II (POTENTIAL).	
FT	DOMAIN	652	666	EXTRACELLULAR (POTENTIAL).	
FT	TRANSFEM	667	687	III (POTENTIAL).	
FT	DOMAIN	688	709	CYTOLASMIC (POTENTIAL).	
FT	TRANSFEM	710	730	IV (POTENTIAL).	
FT	DOMAIN	731	797	EXTRACELLULAR (POTENTIAL).	
FT	TRANSFEM	798	818	V (POTENTIAL).	
FT	DOMAIN	819	834	CYTOLASMIC (POTENTIAL).	
FT	TRANSFEM	835	855	VI (POTENTIAL).	
FT	DOMAIN	856	863	EXTRACELLULAR (POTENTIAL).	
FT	TRANSFEM	864	884	VII (POTENTIAL).	
FT	REPEAT	29	95	SUSHI 1.	
FT	REPEAT	99	156	SUSHI 2.	
FT	DOMAIN	885	991	CYTOLASMIC (POTENTIAL).	
FT	DOMAIN	901	955	COILED COIL (POTENTIAL).	
FT	CARBOHYD	23	23	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	83	83	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	408	408	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	439	439	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	481	481	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	501	501	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	513	513	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	VARSPLIC	1	163	MLLLLVPLRLPLGAGGAOTENATSEGCIIHPWEGGIR YRGLTRDQVKAINFLPVDYIEYVCGEREVGPVKRKCLA NGSWTDMTPSCVRICKSYLTLENGKVLFGGDLPALDG ARVEFCDPDLHLGSSRSVCSOGQSTPKPKQVNRTPH -> MGPGGCTPGWPLPLLLVMAAGVAPWASHSHPLRP HRPVPHPS (IN ISOFORM 1B, ISOFORM 1C AND ISOFORM 1D).	
FT	VARSPLIC	771	801	MISSING (IN ISOFORM 1A, ISOFORM 1B AND ISOFORM 1D).	
FT	VARSPLIC	935	991	KEERSYELRHQLSQRRRLRPPPTPPSGGLPRGPSEP PDRLSCDGSRHLLKY -> VCGDKQPGPVSEGGPLVVP STEV (IN ISOFORM 1D).	
FT	MUTAGEN	247	247	S->A: NO CHANGE IN THE AFFINITY FOR GABA.	
FT	MUTAGEN	268	268	S->A: NO CHANGE IN THE AFFINITY FOR GABA.	
FT	MUTAGEN	269	269	S->A: DECREASE IN THE AFFINITY FOR GABA.	
SQ	SEQUENCE	991 AA;	111533 MW;	012CD293D4B44A2 CRC64;	
Query Match 45.8%; Score 2004; DB 1; Length 991;					
Best Local Similarity 47.5%; Pred. No. 1e-145;					
Matches 385; Conservative 152; Mismatches 219; Indels 54; Gaps 9;					
Qy	24	PHLOGGVAGRPDE	-LHIGGIFPIAGKGWGGQACMPATRLALDDVNKOPNLLPGFKLI	81	
Db	154	PHCVNRRPHSERRAYICALPMS	--GWPGQACQAPVEMALEDDVNSRRDILPDYELK	211	
Qy	82	LHSNDECEPGLGASVYNNLLYKPKMLLAGCSTVCTTVABAAMNLLIVLCYASSP	141		
Db	212	LTHDSKCDPGQATKYELLYNDPIKIILMPGSCSVSTLVAAEARMNLLIVLSGSSP	271		
Qy	142	ALSDKRKFTLTERTHPSATVHNPTRIKMKKFCWSRVAILQOAEVFEISTVEDLENRCME	201		
Db	272	ALSNRQRPFTTERTHPSATVHNPTRIKMKKFCWSRVAILQOAEVFEISTVEDLENRCME	331		
Qy	202	AGVELTQTSFLSDPTDAVNRLLRQDARIIVGLFYVVAARRVCEMYKOOLYGRAHWFF	261		
Db	332	AGIETFRQSFSDPAPVKNLKRQDARIIVGLFYETEARKVCEVYKERLFQKKYWFEL	391		
Qy	262	IGWYEDNMYEVALKABGICTCTVEQMRIAEEGLTTEALMNNQNTTISGMTAEFEHRL	321		
Db	392	IGWYADNWEKT--YDPSINCTVEEMEAVEGHITTEIVMLNPANTRISNWTSGEVEKL	449		
Qy	322	NOALLEEGYDINHRYPE--GYQEAPLAYDAVMSVALAFNPKMTMERITTTGKKSRLDRPTT	378		
Db	450	TKRL-----KRHEETGGFOEAPLAYDAIWAALALANKTSGGGGSGVRLEDENYN	500		

QY	379	DKEIADIYAMNSTQPLGVSQGVAFSSQGDRIALTQIEQMDCKYKELGYDYDTQDNL	438		
Db	501	NOTITDQIYRAMNSSSEFVSGHVYFDASGSRMAWTIEQLQGGYKIGYDSTKODLS	560		
QY	439	WLATEQWIGKVPQDRITVTHVLTSLPLFVCMCTISSGIFVAFALIIFNINWKHRRV	498		
Db	561	WSTDKWIGGSPADQTLVTKTFRFLSOKLFISVSVLSSGLIVLAVCLSENIYNSHVRY	620		
QY	499	IQSSHPVCNTIMLFGVILICLISVLLGIDGRFVSPEEPKICQARAWLLSTGFTLAYGAM	558		
Db	621	IQNSQPNLNLITAVGCSLAAAPFLGLDGVHIGRSQFPFVQCQARLWLLGLGFSIGSM	680		
QY	559	FSKVRVHRTTK--AKTDPKPKVPEWKLYTMVSGLLSIDLVLLSQIFDPLORYLETFF	616		
Db	681	FTK1WVHTVFTKKEKKEWKRTLEPKLYATVGLLVGMVLTALINQIVDPLHRTIETF	740		
QY	617	PLEDPVSTDDIKIRPELEHCEQSNMVLG-----	647		
Db	741	AKEEPKEDI-DVSLPOLEHCCSKKMTWJGELMSFAVSDVQRATVGGSPICVWPAP	799		
QY	648	--LVYGEKGLIVFGLFLAYETRSIKVKQINDSRVYMSIYNNVVLCLITAPVGMVIASQ	705		
Db	800	ESIFYGKGLLLGLGIFLAYETKSVSTEKINDHRAVGMAYINVAVCLITAPVTMILSSQ	859		
QY	706	QDASFAFVALAVIFCCFLSMILLIFVPKVIEWIRHPKDKAESK--YNPDSATSKDEERYQ	763		
Db	860	QDAFAFASLAIVFSSYITLVLFVPMRRLITRGESQETQDTMTKGTSGSTNNNEEKSR	919		
QY	764	KLVTEQLOQLTOKEEIRVLQRQLVER	793		
Db	920	LLEKENRELEKIIAEKEERSVSELRHQLQSR	949		
RESULT 4					
GBR2_HUMAN STANDARD; PRT; 941 AA.					
ID	GBR2_HUMAN	STANDARD;	PRT;	941 AA.	
AC	075899; 075974; 075975; 09UN59; 09UN91; 09P1R2;				
DT	20-AUG-2001 (Rel. 40, Created)				
DT	20-AUG-2001 (Rel. 40, Last sequence update)				
DT	20-AUG-2001 (Rel. 40, Last annotation update)				
DE	GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 2 PRECURSOR (GABA-B				
DE	RECEPTOR 2) (GABA-B-R2) (GB2) (GABABR2) (G PROTEIN-COUPLED RECEPTOR				
DE	51) (GPR 51) (HG20).				
GN	GABBR2 OR GPR51.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 2A).				
RC	TISSUE=Cerebellum;				
RX	MEDLINE=99087321; PubMed=9872316;				
RA	White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H.,				
RA	Barnes A.A., Emson P., Food S.M., Marshall F.H.;				
RT	"Heterodimerization is required for the formation of a functional				
RT	GABA(B) receptor.";				
RL	Nature 396:679-682(1998).				
RN	[2]				
RP	PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2A; 2B AND 2C).				
RC	TISSUE=Brain;				
RX	MEDLINE=20193514; PubMed=10727622;				
RA	Clark J.A., Mezey E., Lam A.S., Bonner T.I.;				
RT	"Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";				
RL	Brain Res. 860:41-52(2000).				
RN	[3]				
RP	SEQUENCE FROM N.A. (ISOFORM 2A).				
RA	Liu M., Parker R., McCrea K., Watson J., Baker E., Sutherland G.,				
RA	Herzog H.;				
RT	"Cloning and characterization of a novel human GABA-B receptor subtype				
RT	with high affinity for GABA and low affinity for baclofen.";				
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.				
RN	[4]				

RC SEQUENCE FROM N.A. (ISOFORM 2A).
RC TISSUE-Hippocampus;
RA Borowsky B., Laz T., Gerald C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RC TISSUE-Fetal brain;
RX MEDLINE=99180236; PubMed=10087195;
RA Ng G.Y.K., McDonald T., Bonner T., Rigby M., Heavens R., Whiting P.,
RA Chateaufort A., Coulombe N., Kargman S., Caskey T., Evans J.F.,
RA O'Neill G.P., Liu Q.;
RT "Cloning of a novel G-protein-coupled receptor GPR 51 resembling GABAB
RT receptors expressed predominantly in nervous tissues and mapped
RT proximal to the hereditary sensory neuropathy type 1 locus on
RT chromosome 9.";
RL Genomics 56:288-295(1999).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2A), AND VARIANTS PHE-628 AND ALA-869.
RC TISSUE-Brain;
RX MEDLINE=99263199; PubMed=10328880;
RA Martin S.C., Russek S.J., Farb D.H.;
RT "Molecular identification of the human GABABR2: cell surface
RT expression and coupling to adenylyl cyclase in the absence of
RT GABABR1.";
RL Mol. Cell. Neurosci. 13:180-191(1999).
RN [7]
RP R1A-R2 INTERACTION.
RX MEDLINE=99175124; PubMed=10075644;
RA Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan R.,
RA Kargman S., Chateaufort A., Tsukamoto N., McDonald T., Whiting P.,
RA Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
RA Bonner T.I., O'Neill G.P.;
RT "Identification of a GABAB receptor subunit, gb2, required for
RT functional GABAB receptor activity.";
RL J. Biol. Chem. 274:7607-7610(1999).
RN [8]
RP R1A-R2 INTERACTION.
RX MEDLINE=20237752; PubMed=10773016;
RA Sullivan R., Chateaufort A., Coulombe N., Kolakowski L.F. Jr.,
RA Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K.,
RA Abramowitz M., O'Neill G.P., Ng G.Y.K.;
RT "Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B))
RT receptors with truncated receptors and metabotropic glutamate
RT receptor 4 supports the GABA(B) heterodimer as the functional
RT receptor.";
RL J. Pharmacol. Exp. Ther. 293:460-467(2000).
CC -1- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES
CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
CC ANTINOCEPTION.
CC -1- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
CC HAPPEN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
CC PLASMA MEMBRANE.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 2A (SHOWN HERE), 2B AND 2C; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN
CC CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND
CC TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORPUS
CC CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, AMYGDALA AND MEDULLA.

CC WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.
CC -1- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC GABA-B RECEPTOR SUBFAMILY.
CC -----
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CC -----
DR EMBL; AJ012188; CAA09942.1; -
DR EMBL; AF056085; AAC63228.1; -
DR EMBL; AF095723; AAC63383.1; -
DR EMBL; AF095724; AAC63384.1; -
DR EMBL; AF095784; AAD30389.1; -
DR EMBL; AF074483; AAD03336.1; -
DR EMBL; AF069755; AAC99345.1; -
DR EMBL; AF099033; AAD45867.1; -
DR InterPro: IPR001828; ANF_receptor.
DR InterPro: IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMR.
DR PRINTS; PR01176; GABABRECEPTR.
DR PRINTS; PR01177; GABAB1RECPTR.
DR PRINTS; PR01178; GABAB2RECPTR.
DR PROSITE; PS00099; PRO-RICH; 1.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; FALSE_NEG.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; FALSE_NEG.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; FALSE_NEG.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Postsynaptic membrane; Coiled coil; Alternative splicing;
KW Polymorphism.
FT SIGNAL 1 41
FT CHAIN 42 941
FT GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR,
FT SUBUNIT 2
FT DOMAIN 42 483
FT TRANSMEM 484 504
FT DOMAIN 505 522
FT TRANSMEM 523 543
FT DOMAIN 544 551
FT TRANSMEM 552 572
FT DOMAIN 573 597
FT TRANSMEM 598 618
FT DOMAIN 619 654
FT TRANSMEM 655 675
FT DOMAIN 676 691
FT TRANSMEM 692 712
FT DOMAIN 713 720
FT TRANSMEM 721 741
FT DOMAIN 742 941
FT DOMAIN 781 819
FT CARBOHYD 90 90
FT CARBOHYD 298 298
FT CARBOHYD 389 389
FT CARBOHYD 404 404
FT CARBOHYD 453 453
FT CARBOHYD 902 927
FT VARSPIC 929 941
FT VARIANT 628 628
FT VARIANT 869 869
FT VARIANT 869 869
FT CONFLICT 6 6
FT CONFLICT 12 12
FT CONFLICT 424 424
FT CONFLICT 941 AA; 105821 MW; 09F1773DB0673C5D CRC64;
FT SEQUENCE

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Query Match      29.5%; Score 1290; DB 1; Length 941;
Best Local Similarity 33.9%; Pred. No. 6.2e-91;
Matches 286; Conservative 170; Mismatches 332; Indels 56; Gaps 18;

Qy 18 LCLTASPHLQGGVACRP-----DELHIGGIPFI---ACKGSGWQGOACMPATRLALDDV 68
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 31 LLLPLAPGAWGARGAPRPPSPSPPLSLINGMLPLTKEVAKGSI--GRGVLPAPVELAIEQI 88
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 69 NKQPNLLPGFKLILHNSDEPCPGGLGASVYNNLLYNKPKMLLAG-CSTVCTTVAEAAK 127
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 89 RNESLLRPF-LDLRLYTECDNAGKLKAFYDAIKYGNPHLMVFGVCSFVSIIAESLQ 147
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 128 MNLIVLCYGASSPALSDDKREPTFLTRHPSATVHNPTRIKLMKFGWRSVAILLOAAEEV 187
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 148 GNNLVOLSFAATTPVLADKKKYPYFERTVPSDNVNPAILKLLKHVQWKRVGFTLTDVQR 207
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 188 FISTVEDLENRCMEAGVEIVTQSFSLSDPTDVRNLRDARLIIVGLFYVVAARRVLCME 247
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 208 FSEVRNDLTGLVGEDIEISTESFSDNPDCTSVKLLKGNDRVRIILGFQDNMAAKVFCCA 267
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 248 YKQOLYGRAHVWFFIAGWEDNWE-VNLKAEGITCTVEOMRTAAEGHLTEALMWNQNNQ 306
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 268 YEENYIGSKYQIIPGWYEPSPWQVHTTEANSSRCURKLLAMEGYIGVDFEPLSKQI 327
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 307 TTISGMTAEFRHRLNQALIEBQYDINHDPYEGYQEAFLAYDAVMSVALAFNKTMERL- 365
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 328 KTISCKTPQOYEREYNNKRSVGPSKFH-----GY-----AYDGIWVIKTLQRAETLH 377
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 366 -TTGKKSURDFTYTKETADEIYAAMNSTQFLGVSGVAFSPGQDRIALTOEQMDIGKY 424
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 378 ASSRHQIQDENYDHTLGRILLNAMNETNFFGVTVGVVFRN-GERMGTIKFTQFQDSRE 436
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 425 EKLGYDQDLNLSLN-TEOWIGKGVPODRTIVTHVLTSLPFCVCTTSSCGIFVA 483
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 437 VAVGEINAVADLEINDIRFQGGSEPPDKTIILQRLKRISLPLYSILSALTILGMIMA 496
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 484 FALIIFNIWKNHRRVITQSHPCVNTIMLFGVILICLSVILLGIDGRFVSPEEYPKICQAR 543
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 497 SAFLFENIKRNQKLIKMSPPYNNLLIILGMLSYASIFLGLDGSFVSEKTFETLCTVR 556
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 544 AWLLSTGFTLAYGMSKVVVRVHRTTKAKTDPKKVEPKWLYVMVSGLLSIDLVILLWS 603
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 557 TWILVGVYTAFAAMFAKTRVHAIFKNVKM-KKKIIRKQKLLVIVGGMLLIDLCILICW 615
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 604 QIFDPLQRYLTFPLE-DPVSTDDIKIRPELEHCESQSNMVLGVYGFGLILVGLF 662
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 616 QAVDPLRLRTVEXYSMEPPDAGR--DISIRPLEHCENHTHWIWLGIYAYKGLMLLFGCF 673
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 663 LAYETRSIKVKOINDSRVYGMSTYNNVVLCLITAPVGMVIASOODASFAPVALAVIFCCF 722
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 674 LAWETRNVSIPALNSKYGMSVYNGVINGIICAAVSFLTRDQPNVQFCIVALVIFCST 733
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 723 LSMLLIFVPKVTEVTRHP-----KDKAESYNDP-SAIKREDEERYOKLVY 767
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 734 IFLCLVFPVKLITRNPDAAATQNRFRFQTONOKEDSKTSTSVTSVNOASTSRLEGLQS 793
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 768 ENEQLQRLITQKEEKIRVLRQLVERGDAKT-----ELNGATGVASAAVATTSQPA 819
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 794 ENHRUMKITELDKDLEVTMQLQDTPPE-KTYIKONHYOELNDILNLTGNTTESTDGGKA 852
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 820 SLIN 823
   | |
Db 853 ILKN 856

RESULT 5
ID GBR2_RAT STANDARD; PRT; 940 AA.
AC O88871: O9QWU2; O9JK36;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
```

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DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 2 PRECURSOR (GABA-B
DE RECEPTOR 2) (GABA-B-R2) (GB2) (GABABR2).
GN GABBR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RX MEDLINE=99087320; PubMed=9872315;
RA Jones K.A., Borowsky B., Tamm J.A., Craig D.A., Durkin M.M., Dai M.,
RA Yao W.-J., Johnson M., Gunwaldsen C.A., Huang L.-Y., Tang C., Shen Q.,
RA Salton J.A., Morse K., Laz T., Smith K.E., Nagarathnam D., Noble S.A.,
RA Branchek T.A., Gerald C.;
RT "GABA(B) receptors function as a heteromeric assembly of the subunits
RT GABA(B)R1 and GABA(B)R2.";
RL Nature 396:674-679(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex, and Cerebellum;
RX MEDLINE=99087322; PubMed=9872317;
RA Kaupmann K., Malitschek B., Schuler V., Heid J., Froestl W., Beck P.,
RA Mosbacher J., Bischoff S., Kulik A., Shigemoto R., Karschin A.,
RA Bettler B.;
RT "GABA-B receptor subtypes assemble into functional heteromeric
RT complexes.";
RL Nature 396:683-687(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=20193514; PubMed=10727622;
RA Clark J.A., Mezey E., Lam A.S., Bonner T.I.;
RT "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";
RL Brain Res. 860:41-52(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RA Borowsky B., Laz T., Gerald C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP RIA-R2 INTERACTION, AND VARIANTS TYR-337 AND PRO-19 INS.
RC TISSUE=Hippocampus;
RX MEDLINE=99102694; PubMed=9872744;
RA Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
RA Kornau H.-C.;
RT "Role of Heteromer Formation in GABA-B Receptor Function.";
RL Science 283:74-77(1999).
CC -1- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES
CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
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CC HAPPEN.
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CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
CC PLASMA MEMBRANE.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN CORTEX, HIPPOCAMPUS, MEDIAL
CC HABENULA, THALAMUS AND CEREBELLUM. COEXPRESSION IS SEEN IN
CC CEREBELLUM.
```


GN GRM8 OR GPRC1H OR MGLURB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEGLINE=97168760; PubMed=9016353;
RA Saugstad J.A., Kinzie J.M., Shinohara M.M., Segerson T.P.,
RA Westbrook G.L.;
RT "Cloning and expression of rat metabotropic glutamate receptor 8
RT reveals a distinct pharmacological profile";
RL Mol. Pharmacol. 51:119-125(1997).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: PROMINENT EXPRESSION IN OLFACTORY BULB,
CC PONTINE GRAY, LATERAL RETICULAR NUCLEUS OF THE THALAMUS, AND
CC PIRIFORM CORTEX. LESS ABUNDANT EXPRESSION INCEREBRAL CORTEX,
CC HIPPOCAMPUS, CEREBELLUM, AND MAMILLARY BODY.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; U63288; AB09537.1; -
DR GCRdb; GCR_1411; -
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF000003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCR_MGR.
DR PRINTS; PR00593; MTABOTROPICR.
DR PRINTS; PR01058; MTABOTROPICR.
DR PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
DR PROSITE; PS00981; G_PROTEIN_RECP_F3_4; 1.
DR PROSITE; PS0259; G_PROTEIN_RECP_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Olfaction.
FT SIGNAL 1 33
FT CHAIN 34 908
FT DOMAIN 34 583
FT TRANSMEM 584 608
FT DOMAIN 609 620
FT TRANSMEM 621 641
FT DOMAIN 642 647
FT TRANSMEM 648 658
FT DOMAIN 659 695
FT TRANSMEM 696 716
FT DOMAIN 717 746
FT TRANSMEM 747 768
FT DOMAIN 769 781
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FT DOMAIN 804 818
FT TRANSMEM 819 843
FT DOMAIN 844 908
FT CARBOHYD 95 95
FT CARBOHYD 298 298
FT CARBOHYD 452 452
FT CARBOHYD 480 480
FT CARBOHYD 565 565
SQ SEQUENCE 908 AA; 101866 MW; FCAB54CB8E3DD915 CRC64;

Query Match 8.3%; Score 361; DB 1; Length 908;
Best Local Similarity 21.0%; Pred. No. 1.3e-19;

RESULT 8
MGR8_HUMAN

Matches 204; Conservative 154; Mismatches 374; Indels 238; Gaps 45;
QY 13 FWIFLLCLLIASPHLQGGVAG-RPD-ELHIGGIFPFIAGKGGOGQAC-----MP 59
DB 22 YWI--LTMMQTHSQEYAHSRVGDGDIILGGLFPVHAKG--ERGVPCCGLKEKGHRL 77
QY 60 ATRLALDDVNKOPNLLPGFKL---IL-----HNSDSECEPL 93
DB 78 AMLYAIQDKPDLLSNITLGVRLDTCSDTYALEQSLTFVQALIEKDASDVKANGD 137
QY 94 GASVYNNLLYNNKPKL--MLLAGCSTVCTTVAEAAKMMNLIVLCYGAGSPALSDRRRPT 151
DB 138 PP-----IFTKPKDISGIVAASSVSIMVANILRLFKIPQISYASTAPELSDNTRVDF 191
QY 152 LFRTHPSATVNPTRIKLKKFGHSRVALLOQAAEEFFISTVEDLENRCME-AGVEIVTRQ 210
DB 192 FSRVPPDSYQQAQAWDIVTALGMNVSTLASSENGYSGVEAFQISREIGGVCAIOSQ 251
QY 211 SFLSDPTDA-----VRNLRQDARIIVGLFVVAARVLCMEYKQOLYGRAHVFFIGW 264
DB 252 KIPREPRGPEFEKIIKRLLETPNARAVIMFANEDDIRILEAAKKLNOSGH---FLWIG- 307
QY 265 YEDNW-----YEVNKAEGITCTVEQMRTAAEG---HLTTEALMWNQNNOTTISGMTA 314
DB 308 -SDSMGSKIAPVQOEETAEAG-AVTILPKRASIDGDFRYSRTLANRRNV-----WFA 360
QY 315 EEPHRLNQALIEGSDYINHDYRPEGY-----QEAPLAY--DAVMSVALAFNMTM 362
DB 361 EFWEENECKLGLSGHGKRNHSHKCTGLERIARDSSYEQEGKQVQFIDAVYSMAVALHNMH 420
QY 363 ERLTTGKKSLL--RFTYTDKEIADEIYAAMNSTQFLGVSQV-VAFSSOGDRIALTOIEQ- 418
DB 421 KERPQYIGLCPRMVTIDGKELLYIRA-----VNFNGSAGTPVTFNENGADAPGRYDIFQY 476
QY 419 MIDGK---YEKLGYYDTOL---DNLSWLNTEQWIGGKVPQDRTVTHVLRVTSUP---- 467
DB 477 QINNKSTYEKIIGHWTNQLHLKVEDMQWANKREH-----THPASCVSLPCKPG 523
QY 468 -----LFVCMCTI-----SSC----- 478
DB 524 ERKKTGVGPCWHCEGEGYNYQVDELSCELCPLDQRPINRTGCQRIPIIKLEHSPW 583
QY 479 ---GIFVA-----FALIIFNWNKHRRVIOSSHPCVNTIMLPGVILCLISVILLGID 527
DB 584 AVVPFVAILGIIATTFVITVFRYN-DTPIVRASGRELSYVLLTGIFLCYSITFLM--- 639
QY 528 GRFVSPEEYPKICQARAWLLSTGFTLAYGAMFSKVMRVHRTTKAK---TDPKKKVEPK 584
DB 640 --IAAPDTI--ICSFRIFLGIMCFSTYALTLTKNRHRIFEQKKSVTAP-KEISPAS 694
QY 585 LYTMVSGLLSIDLVILLSQWIFDP---LQRYLETPLDPVSTDDIKIRPELEHESQOR 641
DB 695 QLVITFSLISVQLLGVFVFWVDDPPHTIIDYGEQRTL-DPENARGVLK-----CDISD 746
QY 642 NSMWGLVYGFKGLILVFGFLAYETRSIKVKQINDSYVMSIYNNVVLCILITAPQMV 701
DB 747 LSLICSL--GYSILLMVTCTVYAIKTRGP-ETFEAKPIGFTMTYTCIIWLAFIPIFG 803
QY 702 IASOODASF---AFVALAVIFCCFLSMILLIFVPKVIEWIRHPKDKAESKYNPDSAIKED 758
DB 804 TAQSAEKMYIQTTTLTVMSLSASVSGLMYPKVIIFHPEQNVQRR----- 852
QY 759 EERYQKLVTEQQLRLITQKEEKIRVLRQLRVERGDAKTELGATGVASAAVATTSQP 818
DB 853 KRSEKAVVTAATMQSKLQKGNDR-----PNGEVK-SEL-----CESLETNVSSTK 897
QY 819 ASLINSAAHA 828
DB 898 TTYISYNSHS 907


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QY 468 -----LFVCMCTI-----SSC----- 478
Db 524 ERKTKVGPCCWCHCEGYNQVDELSCELCPLDORPNMRTGQLPIIKLEHSPW 583
QY 479 ---GIFVA-----FALIIFNIWNKHRRVIOSSHVPVNTIMLFGVILCLISVILLGID 527
Db 584 AVVPFVAILGIIATTFVIVFVRYN-DTPIVRASGRSLSYVLLTGIFLCYSITFLM--- 639
QY 528 GRFVSPPEYPIKQARALLSTGFTLAGMPSKVMVRHRTTKAK---TDPKKKVEPWK 584
Db 640 --IAAPDTI--ICSPRRVFLGLGCMCFSAALLTKTNRIHRIPEQGGKSVTAP-KETSPAS 694
QY 585 LYTWSGLLSIDLVLKSWOIFDPLQRLVLETPLEDPVSTDDIKIRPELEHCESORNSM 644
Db 695 QLVITFSLISVOLLGVFVFWVDDPHIID-----YGEQRTLDPEKARGVLK-CDISDL 749
QY 645 WLGVYGFGLILVFLGFLAVETRSIKVKOINDSRVGVMSIYVNVLCILITAPVGMVIA 704
Db 750 ICSL--GYSILLWCTVYAIKTRGV-ETFNEAKPIGFTMTYTTCIWLAFIPFEGTAQ 806
QY 705 QODASF---AFVALAVIFCCFLSMILLIFVPKVIEWIRHPKDKAESKYNPDSSAISKEDEER 761
Db 807 SAEKMYIQTTTLTVSMLSASVSLGMLYMPKYVYIIIFHPQNVQKR-----KRS 855
QY 762 YOKLVTEQIQRITQKEKIRVLQRILVERGDAGKTELNGCATGVASAAVATTSPASL 821
Db 856 FKAVVTAATMOSKLTQKGNDR-----PNGEVK-SEL-----CESLETNTSSTKTTY 900
QY 822 INSSAHA 828
Db 901 IYSNHS 907

RESULT 9
MGR4_RAT
ID MGR4_RAT STANDARD; PRT; 912 AA.
AC P31423;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.
GN GRM4 OR GPRC1D OR MGLUR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92110002; PubMed=1309649;
RA Tanabe Y., Masu M., Ishii T., Shigemoto R., Nakanishi S.;
RT "A family of metabotropic glutamate receptors.";
RL Neuron 8:169-179(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93332699; PubMed=8338667;
RA O'Hara P.J., Sheppard P.O., Thøgersen H., Venezia D., Haldeman B.A.,
RA McGrane V., Houamed K.M., Thomsen C., Gilbert T.L., Mulvihill E.R.;
RT "The ligand-binding domain in metabotropic glutamate receptors is
RT related to bacterial periplasmic binding proteins.";
RL Neuron 11:41-52(1993).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS. PREDOMINANT
CC EXPRESSION IS SEEN IN THE GRANULE CELLS OF THE CEREBELLUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR6.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M92077; :; NOT_ANNOTATED_CDS.
DR EMBL; M90518; AAA93190.1; :;
DR PIR; JH0563; JH0563.
DR GCRDB; GCR_0352; :;
DR GCRDB; GCR_0363; :;
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMR.
DR PRINTS; PR00593; MTABOTROPICR.
DR PRINTS; PR01054; MTABOTROPICR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS00982; G_PROTEIN_RECEP_F3_4; 1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 912 METABOTROPIC GLUTAMATE RECEPTOR 4.
FT DOMAIN 33 587 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 588 610 I (POTENTIAL).
FT DOMAIN 611 624 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 625 645 II (POTENTIAL).
FT DOMAIN 646 656 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 657 675 III (POTENTIAL).
FT DOMAIN 676 699 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 700 720 IV (POTENTIAL).
FT DOMAIN 721 750 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 751 772 V (POTENTIAL).
FT TRANSMEM 773 785 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 786 808 VI (POTENTIAL).
FT DOMAIN 809 821 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 822 847 VII (POTENTIAL).
FT DOMAIN 848 912 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 484 484 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 569 569 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 124 124 Q -> R (IN REF. 2).
SQ SEQUENCE 912 AA; 101818 MW; 336430EF19B4B577 CRC64;

Query Match 8.2%; Score 356.5; DB 1; Length 912;
Best Local Similarity 18.9%; Pred No. 2.8e-19;
Matches 177; Conservative 164; Mismatches 374; Indels 221; Gaps 36;

QY 5 MTSDBGAVTFW--IFLLCLIAS-----PHLQGGVAGRP-----DELHIGGFPIAGK 48
Db 1 MSCKGGWAWWARIPLCLLLSLYAPWVPSLGLKPKGPHMNSIRIDGDTLGLGLFPVHGR 60
QY 49 GWWQGGQAC-----MPATRLADDVNKPNLLPGFKL----- 80
Db 61 G--SEKACGKELKKEGIHRLAFLDRLINDDPDLPLNITLGLARILDTCSRTHALEQ 118
QY 81 -----ILHSNDECEPGLGASVWVLLYNNKPKMLLAGC--STVCTTVAEAKWNL 131
Db 119 SLTFVQALIEKDGTEVRCGGGPP-----IITKPVVGVIGASGSSVSIMVANILRFKI 174
QY 132 IVCYGCASSPALSDRKRPFTLFRTHPSATVHNPNTRIKMKFGWSRVAIL-----QQA 184
Db 175 PQISYASTAPDLSDNSRYDFRSRVVPSDTYQAQAMVDIVALKKNYVSTLASESGYSG 234
QY 185 EEVFISTVEDLENRCMBAGVEIVTQSFSLSDPTDAVRLRRQDARIIVGLFYVVAARVL 244

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Db 235 VEAFTQKRENGVCIAQSVKIPREPKTGEFDKIKRLLTSSNARGIILIFANEDDIRVL 294
Qy 245 CEMYKQYLGRHVHVFQWYEDNM-----YEVNLKAEQ-ITCTVEQMRIAAGHLFT 296
Db 295 EAARRANQTGH---EFWMG--SDSMGSKGAPVLRLEVEAGAVTILPKRMSVRGFDYFS 349
Qy 297 EALMWNQNOTTISGMTAEFRHLNQALIEGYDI----NHDYEP--GYQE---APLA 347
Db 350 SRTLDNNRRNIWFAEFWEDNFCKLSRHALKKGSHIKCTNRERIGQDSAYEGKGVQV 409
Qy 348 YDAVNSVALAFNKTMRLELTGKKSRLDFTYTKEDIADEIYAAMNSQFGLVSG-VVAFSS 406
Db 410 IDAVYAMGHALHAMDLCPRVGL--CPRMDVDGTQLLKIRNVNFSGIAGNPVTFNE 467
Qy 407 QGDRIALTQIEOMIDKYEKLYGYDTQLDN-----LSW-----LNTEQWIGKVP 451
Db 468 NGD-----APGRYD---IYQVLRNGSAEYKVGISWTDLHLRIERMQWPGSGQ 514
Qy 452 QDRTIVT-----HVLRT----- 463
Db 515 LPRSCSLPCQPGERKKTVMGACCHCEPCTGYQYQVDRYTKCTCPYDMRPTENRTSCQ 574
Qy 464 -----VSLPLPVCMTISSCGIFVAFALIIENIWNKHRRVIOSSHVPVCNTIM 510
Db 575 PIPVYKLEWDSWAPVLPFLAVVGAAT-LFVVVTFVRYN----DTPIVKASGRELSYVL 629
Qy 511 LFGVILICISVILLGIDGRFVSPEEPKICQARAWLLSTGFTLAYGAMFSKVMVRHRTT 570
Db 630 LAGIFLCYATTELM-----IAEPD--LGTCSLRRIFELGLGMSISYAAALLTKNRIYFE 682
Qy 571 KAK--TDPKPKKVEPKLWTMWSGLSIDLVLSWIFDPQLRYLFTFPLEDVSTDDI 628
Db 683 QGKRSVAPRFTSPASQLAITFILLISQLLGICVWFVDPSSHVD---FQD--QRTLDP 737
Qy 629 KIRPELEHESORNWMLGLVYGFGLILVFLFLAYETRSIKVKQINDSRYVGMYSYV 688
Db 738 RFAPGVLKCDI--SLSLCLILGYSMLLVTCTVYAIKTRGVF-EFTNEAKPIGFTMYTT 794
Qy 689 VVLCITAPVGMVIAQQDASFAFV-----ALAVIECCFLSMILLIFVPKVIEWIRHPKDK 743
Db 795 CIVWLAFTPI--FFGTSQSDAKLYIOTITLTVSVLSASVSLGMLYMPKYIILFHPQON 852
Qy 744 AESKNPDSAISKEDEERYQKILTENEOQLRLITQK 779
Db 853 VPKR-----KRSLKAVVTAATMSNKFQK 876

RESULT 10
MGR8_MOUSE STANDARD; PRT; 908 AA.
AC P47743;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
GN GRM8 OR GPRC1H OR MGLUR8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Retina;
RX MEDLINE=95239344; PubMed=7722646;
RA Duvoisin R.M., Zhang C., Ramonell K.;
RT "A novel metabotropic glutamate receptor expressed in the retina and
RL olfactory bulb."
RL J. Neurosci. 15:3075-3083(1995).
CC -!- IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC -!- ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN OLFACTORY BULB,
```

```
CC ACCESSORY OLFACTORY BULB, AND MAMMARY BODY. WEAKER EXPRESSION
CC IN THE RETINA, AND IN SCATTERED CELLS IN THE CORTEX AND HINDBRAIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U17252; AAA68149.1; -.
CC GDB; GCR1712; -.
CC MGD; MGI:1351345; Gprclh.
CC InterPro; IPR001828; ANF_receptor.
CC InterPro; IPR000337; GPCR_Mgr.
CC Pfam; PF00003; 7tm_3; 1.
CC Pfam; PF01094; ANF_receptor; 1.
CC PRINTS; PR00248; GPCRMR.
CC PRINTS; PR00593; MTABOTROPICR.
CC PRINTS; PR01058; MTABOTROPICR.
CC PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
CC PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
CC PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
CC PROSITE; PS0259; G_PROTEIN_RECP_F3_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
CC Multigene family; Olfaction.
CC SIGNAL 1 33 POTENTIAL.
CC CHAIN 34 908 METABOTROPIC GLUTAMATE RECEPTOR 8.
CC DOMAIN 34 583 EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 584 608 I (POTENTIAL).
CC DOMAIN 609 620 CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 621 641 II (POTENTIAL).
CC DOMAIN 642 647 EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 648 668 III (POTENTIAL).
CC DOMAIN 669 695 CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 696 716 IV (POTENTIAL).
CC DOMAIN 717 746 EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 747 768 V (POTENTIAL).
CC DOMAIN 769 781 CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 782 803 VI (POTENTIAL).
CC DOMAIN 804 818 EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 819 843 VII (POTENTIAL).
CC DOMAIN 844 908 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 95 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 298 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 452 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 480 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 565 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 908 AA; 101413 MW; 4CDD9D35827ED41F CRC64;
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Query Match 8.1%; Score 355; DB 1; Length 908;
Best Local Similarity 21.0%; Pred. No. 3.6e-19;
Matches 200; Conservative 159; Mismatches 390; Indels 204; Gaps 44;

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Qy 13 FWIFLLCLLIASPHLOGGVAG-RPD-ELHGGIFPAGKGGWGGQAC-----MP 59
Db 22 YWI--LTMWORTHQSEYAHISRLDGDIIILGLFLPVHAKG--ERGVPCGDLKKEGHIHLE 77
Qy 60 ATRLALDDVNKPNLLPGFKL---IL-----HSNDSECEPGL 93
Db 78 AMLYADQTNKDPDLLSNITLGVRLDTCRSRTYALEQSLTFVQALIEKXADSDVRCAGD 137
Qy 94 GASVMYNNLLNKPQKL--MLLAGCSTVCTTVAEAAKMNWNLIVLCYGASSALSDRRKFT 151
Db 138 PP-----IFTKPDKISGVIGAAASSVIMVANILRLFKIPQISYASTAPELSDNTRYDF 191
Qy 152 LFRTHPSATVINPTRIKMKFGNSRVAILQAAEEVFISTVDELENRCME-AGVEIVTRQ 210
Db 192 FSRVVPDPSYQAQAMVDIVTALGNVYVSTLASEGNYGESGVFAFTQISREIGVCVCAQSQ 251
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FT DOMAIN 611 624 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 625 645 II (POTENTIAL).
FT DOMAIN 646 656 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 657 675 III (POTENTIAL).
FT DOMAIN 676 699 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 700 720 IV (POTENTIAL).
FT DOMAIN 721 750 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 751 772 V (POTENTIAL).
FT DOMAIN 773 785 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 786 808 VI (POTENTIAL).
FT DOMAIN 809 821 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 822 847 VII (POTENTIAL).
FT DOMAIN 848 912 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 484 484 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 569 569 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 912 AA; 101867 MW; 4A2F36E63A2EAF5A CRC64;
Query Match 8.18; Score 353; DB 1; Length 912;
Best Local Similarity 18.5%; Pred. No. 5.2e-19;
Matches 169; Conservative 179; Mismatches 371; Indels 196; Gaps 38;
QY 13 FWIFL-ICLIAS-----PHLOGGVAGRP-----DELHIGGIFPIAGKGGWGGQAC 57
Dy 10 WVARLPCLLLSLXGPMWSSLSGRPKGPHMNSRIDGDTITGLGFPVHGRG--SEGKPC 67
QY 58 -----MPATRLADVDNKPQNLPGFKL-----IL 82
Dy 68 GELKKEGIHRLEAMLFDLRINDPDLNITLGLARILDTCSRTHALEOSLTFVQALI 127
QY 83 HSNDSCEPGLGASVMNLLYNKPKMLLAGC--STVCTTVAEAAKMNLLVLCYGASS 140
Dy 128 EKDTEVRCGGPP-----IITKERVGVIGASCVSVMANILRLFKIPOISYASTA 183
QY 141 PALSDRKRFPTLFTHPSATVHNTPRIKMKKQWSRAIL-----QOAEVEFISTVE 193
Dy 184 PDLSDNSRYDFFSRVPSDVTQAQAMVDIVRAKWNVYSTVASEGSGYSGVEAFIQSR 243
QY 194 DLNRCHEAGVEIYVROSFLSDPTDVRN-LRQDARIIVGLFYVVAARRVLCMYKOOL 252
Dy 244 EDGGVCIAQSVKI-PRPKAGEFDKIRRLLETNSARAVIIFANEDDRIYRLVEAARRAQ 302
QY 253 YGRAHVWFFIGWYEDN-----YEVNKAEG-ITCTVEOMRIAAEGHLLTEALMNQN 304
Dy 303 TGH---FFWVG--SDSGSKIAPVHLHLEVAEGAVTILPKRMSVRGDFRYSRTLDNRR 357
QY 305 NOTTISGMTAEERHRLNQAIEEGYDI-----NHDTYPE--GYQE--APLAYDAVWSVA 355
Dy 358 RNIWFAEFWEDNPHCKLSRHALKSGSHVKKCTNRERIGQDSAYBOEGKVQFVIDAVYANG 417
QY 356 LAFNKWERTTGTKKSRDFTYDKEIADEIYAAMNSQFGLVSG-VVAFSSQGD--RI 411
Dy 418 HALHAMRDLCPRVGL--CPRMDPVDGTQLLVKIRNVNFSGIAGNPVTFNENGDPGRY 475
QY 412 ALTOIEQIMID-GKYEKLG-----YVDQDNLNLSWLTQEWIGKV-----PQDR----- 454
Dy 476 DIYOYQLRNDSAEYKVGWTDHHLRIERHMHVPGSQQLPRSCSLPCQGERKKTVKG 535
QY 455 -----TIVTHVLRT-----VSUPLFLVC 471
Dy 536 MPCWCHEPCTGYQYQVDRYCTKCTPDMRPTENTGCRPTIPIKLEWGSWAVLPLFLA 595
QY 472 MCTISSCGIFVAFALIIENIWNKHRRVIOSSHPCVNTIMLFGVILCLISVLLGIDGRFV 531
Dy 596 VVGIAAT-LFWITFVRYN-----DTPIVKASGRELSYVLLAGIFCYATTFLM-----IA 645
QY 532 SPEYKICQARWLLTGTFTLAYGAMFSKVRVHRFTTKAK--TDPKKKVEPKWLYTMV 589
Dy 646 EPD--LGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFPEQGRKRSVAPRFTISPSOLAIT 703

QY 590 SGLLSIDLVLISQIFDPLQRYLETPLPDDVSTDDIKIRPELEHESQNSMMWLGIV 649
Dy 704 FSLISQLLGICVWFVVDPSHVVDD---FQD--QRTLDPRFARGVLKCDI--SDLSLICL 756
QY 650 YGFKGLILVFLFLAYETRSIKVKQINDSRVGMISYVNVVLCILITAPVGMVIAQQDAS 709
Dy 757 LGYSMLLVMTCTVAIKTRGVP-ETPNEAKPIGFTMTTTCIVWLAFIPI--FFGTSQSD 813
QY 710 FAFV-----ALAVIFCFLSMLLIFVPKIVIEVIRHPKDKAEKYNPDSSAISKEDEERYQK 764
Dy 814 KLYIQTTTLTVSVSLSASVSLGMLPKVYIILFHPQNVPKR-----KRSLK 861
QY 765 LVTENEQQLRLITQK 779
Dy 862 AVVTAATMSNKFQK 876
RESULT 13
MGR7_RAT ID MGR7_RAT STANDARD; PRT; 915 AA.
AC P35400;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR.
GN GRM7 OR GPRC1G OR MGLUR7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX MEDLINE=94117433; PubMed=8288585;
RA Okamoto N., Hori S., Akazawa C., Hayashi Y., Shigemoto R.,
RA Mizuno N., Nakanishi S.;
RT "Molecular characterization of a new metabotropic glutamate receptor
mglur7 coupled to inhibitory cyclic AMP signal transduction.";
RL J. Biol. Chem. 269:1231-1236(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Olfactory bulb;
RX MEDLINE=94195260; PubMed=8145723;
RA Saugstad J.A., Kinzie J.M., Mulvihill E.R., Segerson T.P.,
RA Westbrook G.L.;
RT "Cloning and expression of a new member of the L-2-amino-4-
phosphonobutyric acid-sensitive class of metabotropic glutamate
receptors.";
RL Mol. Pharmacol. 45:367-372(1994).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: WIDELY DISTRIBUTED THROUGHOUT THE BRAIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR4.
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CC -----
CC EMBL; D16817; BAA04092.1; -;
CC EMBL; U06832; AAA20655.1; -;
CC GCRDb; GCR_0945; -;
CC GCRDb; GCR_0946; -;
CC InterPro; IPR001828; ANF_receptor.
CC InterPro; IPR000337; GPCR_Mgr.
CC pfam; PF00003; 7tm_3; 1.
CC pfam; PF01094; ANF_receptor; 1.
CC -----

DR PRINTS: PR00248; GPCRMRGR.
 DR PRINTS: PR00593; MTABOTROPICR.
 DR PRINTS: PR01057; MTABOTROPICR.
 DR PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
 DR PROSITE; PS00982; G_PROTEIN_RECP_F3_4; 1.
 DR PROSITE; PS00983; G_PROTEIN_RECP_F3_5; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Multigene family; Olfaction.
 FT SIGNAL 1 32
 FT CHAIN 33 915
 FT DOMAIN 33 590
 FT TRANSMEM 591 615
 FT DOMAIN 616 627
 FT TRANSMEM 628 648
 FT DOMAIN 649 654
 FT TRANSMEM 655 675
 FT DOMAIN 676 702
 FT TRANSMEM 703 723
 FT DOMAIN 724 753
 FT TRANSMEM 754 775
 FT DOMAIN 776 788
 FT TRANSMEM 789 810
 FT DOMAIN 811 825
 FT TRANSMEM 826 850
 FT DOMAIN 851 915
 FT CARBOHYD 98 98
 FT CARBOHYD 458 458
 FT CARBOHYD 486 486
 FT CARBOHYD 572 572
 FT SEQUENCE 915 AA; 102231 MW; F28AFC4C6454A6C2 CRC64;

Query Match 8.1%; Score 353; DB 1; Length 915;
 Best Local Similarity 21.2%; Pred. No. 5.2e-19;

Matches 206; Conservative 156; Mismatches 320; Indels 290; Gaps 50;

Qy 17 LCLIA-----SPH---LOGVAGRPDELHIGFIPPIAGKGGWGGQAC----- 57
 Db 24 LLCVLAAAARGOEMYPHSHIRIEGDT-----LGLLFPVHAKG--PSGVPCGDKREN 74
 Qy 58 ---MPATRLALDDYKONPLPGFKL---IL-----HNSDS 87
 Db 75 GHRLEAMLYALQDINSDDPILNVTLGARILDTCSDRYALEQSLTFVQALLQKDTSDV 134
 Qy 88 ECEPGLGASVMYNNLYNPKQLMLLAGC---STVCTTVAEAAKMNILVLCYGASSPALSD 145
 Db 135 RCTNGEPP-----VFVKEKVVGVIGASSSVSINVANILRLFOIPQISYASTAPELSD 188
 Qy 146 RKRFTLFTPHSATVHNPTRIKMKFGNSRVAILQQAEEVISTVEDLENRCMEAGVE 205
 Db 189 DRYDFSRVPPDSFQAQAMVDIVKALGN-----YVSTLAS-EGSYGKGE 236
 Qy 206 IVTROSLDPTDAVRLR---RQDA---RIIVGLFVVVAARRVLC-----EMVKKQL 252
 Db 237 SETQISKEAGGICAGIARIPQERKDTIDFDRIKOLLDTPTNSRAVIFANEDIKQIL 296
 Qy 253 YG--RA-HWFFIGVYEDNW-----YEVNLKAEITCTVEOMIAAEG---HLTTEAL 299
 Db 297 AAKRADQVGHFLWGSDSWGSKINPLHQHEDIAEG-AITIQKRAVEGFDAYFTSRTL 355
 Qy 300 -----MW-----NNQNTTISGMTAEF-RHRLNQALIEEGYDINHRYPEGYOEP 345
 Db 356 ENNRNVWFAEYWEENFNCKLTISGSKEDTKRGTQERI--GKDSNYEQ--EG--KVQ 409
 Qy 346 LAYDAVSVLAFNKTMRFTT-----GKSLURDTYTDKETADEIYAMNS 392
 Db 410 FVIDAVYAMAHALHNNKDKLCADYRGVCPMEQAGKLLKYIRHVN----- 456
 Qy 393 TOFLGVSGV-VAFSSOGDRIALTOIQEMIDGKYEKLGYYDTQLDNLWS-----L 440
 Db 457 ---FNGSAGTPVFNKNGD-----APGRYDIFQYQTTNTNPGYRLIGOWTDELQ 504

Qy 441 NTE--QWIGG--KVPO-----DRIVTH-- 459
 Db 505 NIEDMONGKGVREIPSSVCTLPCKPQQRKTKQKTPCWCPCDGYQYQDEMTCOHCP 564
 Qy 460 -----VLRT-----VSLPLFVCMCTISSCGIFEAFAIIFNWNKRR 497
 Db 565 YDORPNERTGCCNIPKLEWHSPWAVIPVFLAMGLIAT-IFVMATFIRN---DTP 619
 Qy 498 VIOSSHPCVNTIMLFVGIICLSVILLIDGRFVSPEYKICQARAWLLSTGFTLAYGA 557
 Db 620 IVRASGRELVSLLTGIFLCVITFLM-----IAKPD--VAVCSFRVRFLGCMCISYAA 672
 Qy 558 MFSKVRVHRFTKAK---TDPKKKVPWKLYTHVSGLLSDVLVLLSQQIFDPQLRVLE 614
 Db 673 LLTKNRIYRIFEQGKKSVTAP-RLISQTSOLATSSISVQLLGVTWFGVDPNNIID 731
 Qy 615 TPLEDDPVSTDDKIRPELHCHESQNRNMMGLVYFGKLLVFLFLAYETRSIKVKQ 674
 Db 732 ----YDEHKTMPQARGVLK-CDITDLOIICSL--GYSILLMVTCTVYAIKTRGVP-EN 783
 Qy 675 INDSRYVGMISYNNVVLCLITAPVGMVIAOODASFAFV-----ALAVIFCCFLSMLLIF 729
 Db 784 FNEAKPIGFTMYTTCIVMLAFIPI--FFGTAQSAEKLYIQTTLTISMNLSASVALGMLY 841
 Qy 730 VPKEVIVIRHPKKAESKYNPDSAISKEDEERYOKLYTENEOQLORLITQKEKIRVLQR 789
 Db 842 MPKVYIIIFHELPNVQKR-----KRSFRAVVTAAATMSSRLSHKPSDR----- 883
 Qy 790 LVERGDAKGTEL 801
 Db 884 --PNGEAK--TEL 892

RESULT 14
 ID MGR6_RAT STANDARD; PRT; 871 AA.
 AC P35349;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 6 PRECURSOR.
 GN GRM6 OR GPRC1F OR MGLUR6.
 OS Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Retina;
 RX MEDLINE=93280152; PubMed=8389366;
 RA Nakanishi S.;
 RA "Molecular characterization of a novel retinal metabotropic glutamate receptor mGLUR6 with a high agonist selectivity for L-2-amino-4-phosphonobutyrate.";
 RT J. Biol. Chem. 268:11868-11873(1993).
 CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: RESTRICTEDLY EXPRESSED IN THE INNER NUCLEAR LAYER OF THE RETINA.
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN-COUPLED RECEPTORS. SPONGEST, TO MGLUR4.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL: D13963; BAA03066.1; -
DR PIR: A46742; A46742.
DR GCRdb; GCR_0623; -
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCR_MGR.
DR PRINTS; PR00593; MTABOTROPICR.
DR PRINTS; PR01056; MTABOTROPICR.
DR PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
DR PROSITE; PS00259; G_PROTEIN_RECP_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Vision.
FT SIGNAL 1 18
FT CHAIN 19 871
FT DOMAIN 19 579
FT TRANSSEM 580 602
FT DOMAIN 603 616
FT TRANSSEM 617 637
FT DOMAIN 638 648
FT TRANSSEM 649 667
FT DOMAIN 668 691
FT TRANSSEM 692 712
FT DOMAIN 713 742
FT TRANSSEM 743 764
FT DOMAIN 765 777
FT TRANSSEM 778 800
FT DOMAIN 801 813
FT TRANSSEM 814 839
FT DOMAIN 840 871
FT CARBOHYD 290 290
FT CARBOHYD 445 445
FT CARBOHYD 473 473
FT CARBOHYD 561 561
SQ SEQUENCE 871 AA; 95089 MW; 9F70B4D6A13B186D CRC64;

Query Match 7.6%; Score 334.5; DB 1; Length 871;
Best Local Similarity 20.3%; Pred. No. 1.3e-17;
Matches 180; Conservative 158; Mismatches 350; Indels 199; Gaps 39;

QY 11 VTFWIF---LLELIASPHLOQGVAGRPDELHTGIFPIAGKGGWGGQAC----- 57
DB 11 LAWLSSQAGIACGAGSVRLAGG-----LTGLGFPVHARGA--AGRACGALKKEQGVH 61

QY 58 -MPATRIALDDVNKOPNLLPGFKLLIHSNDSECE-----PGLGA 95
DB 62 RLEAMLYALDRVADPELLPGVRLGARLLDT-CSRDVYALEQALSVPQALIRGRGDGEA 120

QY 96 SV-----MYNLLYNKPKMLLAG--CSTVCTVYAEAKMKNLIVLCYCASSPALSDDR 148
DB 121 SVRCPGVPPLRSAPPERVAVVGASSVSMVANLRLFAIPQISYASTAPELSDSTR 180

QY 149 PPTLFRTHPSATVNPTRIKMKKGRSVAIL-----QCAEEVFISTVEDLENKRCME 201
DB 181 YDFSRVPPDSYQAQAMDIVRALGNVYSTLASEGNYGESGVEAFVLSREAGGVCTA 240

QY 202 AGVEIVTRQSFSLDPTDAVRNLR---QDARIIVGLFVVAARRVLCMYKQOOLYGRAH 257
DB 241 QSIKIPREPCK---PGEPHKVIIRLMETPNARGIIIFANEDDIRRVLEATRQANLGH-- 294

QY 258 VWFIFGHWEDNWE-----VNLKARGI-TCIVQWRIAAEG---HLTTEALMNQNNQIT 308
DB 295 -FLWVG--SDSWGSKISPLNLEEEAVGAILTPKRASIDGDFQYFMTFSL---ENNREN 348

QY 309 ISGMTAEERHRLNQAILEEGYD-----INHDYPEGVQAPLAYDAVWSVA 355
DB 349 I--WFAEFWEENFNCKLTSSGGQSDDRKCTGEBRIGODSAYEGEGKQVQFVIDAVYIA 406

QY 356 LAFNKTMERLTGKKSL-RDFTYTDKEIADEIYAAMNSTQFLGSGV-VAFSSQGD---R 410

DB 407 HALHMQALCPGHTGLCPAMEPTD---GRLLHVIKRAVRENGSAGTPVWFENEDAPGR 463
QY 411 IALTQIE---QMIIDGKYELGY--DFOLDNLNLWNTQWIGG--KVPQDRTIV----- 457
DB 464 YDIFQYQATNGSASSGGYQAVQWAEALRLD---MEVLRWSGDPHPVPPSCSLPCGPG 519
QY 458 -----THVLR-TVSLPL 468
DB 520 ERKMWAGVPCCHCEACDGYRFQVDEFTCEACPGDMRPTPNHTGCRPTPVVRLTWSSPW 579
QY 469 FVCMCTISSCGIFVAFALIIFENINKNHRRVIOSSHPVQNTIMFGV-IICLISVLLIGD 527
DB 580 AALPLLAVLIGIMATTTIMATFMHNDTPIVRASGRELSYVLLTGIFLIYAITFLMVA-- 637
QY 528 GRFVSPEYPRKICQARAWLLSTGFTLAYGAFMSKVRVHRFTTKAK--TDRKPKKEVPKWL 585
DB 638 -----EPCAICAARLLLGTTLSYALLTKNRIYRIFEQGRKSRVTPPPFISPTSQ 691
QY 586 YTMVSGLLSIDVILLWQIFDPLQRYLETPTPLEDPVSTTDDIKIRPELEHCESSRNMW 645
DB 692 LVITFGLTSLQVGVIAWLGAPPHSVID---VEEQRTVDPEQARGVLK-CDMSDLSL- 745
QY 646 LGLVYGKGLLIVFGLAYETRSIKVQINDSRVGVSIYNNVVLCLITAPVGMVIAQ 705
DB 746 IGCL-GYSLLLMVTCTVYAIKARGVP-ETFNKAPDGTMTYTCIILAFVPI--FFGTA 801
QY 706 QDASFAFV-----ALAVIFCCFLMLLIFVPKIEVIRHPKDKAESK 747
DB 802 QSAEKIIVQITTLIVSLSLASVSLGMLYVPKTYVILFHPQONVQR 848

RESULT 15
MGR3 RAT STANDARD; PRT; 879 AA.
AC P31422; 1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 3 PRECURSOR.
GN GRM3 OR GPRC1C OR MGLUR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92110002; PubMed=1309649;
RA Tanabe Y., Masu M., Ishii T., Shigemoto R., Nakanishi S.;
RT "A family of metabotropic glutamate receptors.";
RL Neuron 8:169-179(1992).
CC -|- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -|- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS. PREDOMINANT
CC EXPRESSION IS SEEN IN THE NEURONAL CELLS OF THE CEREBRAL CORTEX,
CC DENTATE GYRUS, AND GLIAL CELLS THROUGHOUT BRAIN REGIONS.
CC -|- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR2.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M92076; -; NOT_ANNOTATED_CDS.
DR PIR; JH0562; JH0562.
DR GCRdb; GCR_0362; -.

DR InterPro: IPR001828; ANF_receptor.
DR InterPro: IPR000337; GPCR_Mgr.
DR Pfam: PF00003; 7tm_3; 1.
DR Pfam: PF01094; ANF_receptor; 1.
DR PRINTS: PR00248; GPCRMR.
DR PRINTS: PR00593; MTABOTROPICR.
DR PRINTS: PR01053; MTABOTROPICR.
DR PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE: PS02059; G_PROTEIN_RECEP_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family.
FT SIGNAL 1 22
FT CHAIN 23 879
FT DOMAIN 23 576
FT TRANSMEM 577 599
FT DOMAIN 600 613
FT TRANSMEM 614 634
FT DOMAIN 635 645
FT TRANSMEM 646 664
FT DOMAIN 665 688
FT TRANSMEM 689 709
FT DOMAIN 710 734
FT TRANSMEM 735 756
FT DOMAIN 757 769
FT TRANSMEM 770 792
FT DOMAIN 793 802
FT TRANSMEM 803 828
FT DOMAIN 829 879
FT CARBOHYD 209 209
FT CARBOHYD 292 292
FT CARBOHYD 414 414
FT CARBOHYD 439 439
SQ SEQUENCE 879 AA; 98959 MW; 3E5965EDD5E6DEED CRC64;

Query Match 7.6%; Score 333; DB 1; Length 879;
Best Local Similarity 20.6%; Pred. No. 1.7e-17;
Matches 180; Conservative 132; Mismatches 313; Indels 250; Gaps 39;

Qy 36 ELHIGGIPIAGKGGWGOAC-----MPATRALDDVNKOPNLLPGFKLIHS 84
Db 38 DLVLGGLFPINEKG---TGTEECGRINEDRGIORLEAMLFDAIDKNDYLLPGVKLGVI 95
Qy 85 NDS-----ECEPGLGASVMYNNLYNKKPKMLLAGC-- 115
Db 96 LDTCSRDTYALQSLFVPRASLTKYDEAYMCPDG-----SYAIQENIP---LLIAGVIG 147
Qy 116 ---STVCTTVAABAAMNLIIVLCYGASSPALSDRKRFPPTLFRTHPSATVHNPTRIKLMKK 172
Db 148 GSYSSVSIQVANLLRLFQIPQISYASTSAKLSKSDRYDFARTVPPDFYQAKAMAEILRF 207
Qy 173 FCWSRAVILQQAEEVFISTVEDE-----NRCMEAGVELIVTQSFSLDPTDAVRN-LRR 225
Db 208 FNMTYSTVASEGDYGETGIEAFQEARLNICI-ATAEKVGRSNIRKSYDSVIRELLOK 266
Qy 226 ODARIIVGLF-----YVVAARRVLCMEYKQLYGRAHVWPFICGYEDNWEVNLKAE 277
Db 267 PNARVVV-LFMRSDDSRELIAANRV-----NASFTWV-----ASDCWG-----AQE 307
Qy 278 GITCTVEQMRIAAGHLTTPEAL-----MWNQNNQTTIS 310
Db 308 SI---VKGEHVAYGAITLELASHPVQRDFYFQSLNPNYNNHRNPWFRDPWEQFQCSLQ 364
Qy 311 GMTAEFRHRLNQAILEEGYDINHDPYEGYOEAPLAY--DAVSVALAPNKTWERLTTC 368
Db 365 -----NKRNRHQVCDKHLAIDSSNYE---QESKIMFVNVNAVYAMAHALHKMQRTLCPN 414
Qy 369 KKSRLDF--TYTDKEIAEIIYAAMNSTQFL----GVSGVVAFFSSQGDRIALTQI--EQMI 420
Db 415 TTKLCDAMKILDGKLYKEYLLKINFTAPNPNKMGADSIYKFDFTFGDGMGRYVNFNLQQT 474

Qy 421 DGKYE--KLGYY-----DTQDNLSSM-----LNTQ-----WI----- 446
Db 475 GGKYSYLYKVGHWAEITLSLDVDSIHWSRNSVPTSCSDPCAPNEMKNMQPGDVCCWICIPC 534
Qy 447 -----GKVP-----QDRTIVTHVLRVTSPLFVCMC 473
Db 535 EPEYLVDEFTCMDGPGQWPTADLSGCYNLPEDYIKWEDAWAICPV--TIACLGFLCTC 592
Qy 474 TISSCGIFAFALIIIFNINWKKHRR---VIOSSHVPCVNTIMLFGVIICILISVILLGIDGRF 530
Db 593 -----IVITVFIKHNNTPLVKASGRELC-YILLFGVSLSYCMTF-----F 631
Qy 531 VSPPEYKICQARAWLLSTGFTLAYGAMFSKVRVHRETTAKTDPK--KVEPHKLYTM 588
Db 632 FIAKPSVICALRRLGLGTSAICYALLTKTNCIARIFDGVKNKAQRPKFISSSQVFI 691
Qy 589 VSGLLSDDLVLILLSQWIFDP--LQRYLETFFLEDVPVSTDDIKIRPELEHCESSQNSMWL 646
Db 692 CLGLILVQIVMVSVMWLLILETPGTRY--TLP-----EKRETVILKCNVKDSSMLI 739
Qy 647 GLVYGFKGLILVFLGLFAYETRSIKVKQINDSRVGMYSIYVNVVLCITAPVGMVIAQQ 706
Db 740 SLTYDV--VLVILCTVYAFKTRKCP-ENFNEAKETGFTMYTTCIIWLAFPIFYVTSDDY 796
Qy 707 DASFAFVALAVIFCCFLSMLLIFVPKVIETVIRHPK 741
Db 797 RVQTTMCISVSLSGFVVVLGCLFAPKVHIVLFQPO 831

Search completed: April 30, 2002, 10:16:52
Job time: 224 sec

QY 262 IGWYEDNWYEYNLKAEGITCTVEQNRIRAAEGHLTTEALMWNQNNQTTISGMTAEFRHRL 321

[illegible]

Query Match	10.4%	Score 457;	DB 2;	Length 402;
Best Local Similarity	29.9%	Pred. No. 1e-27;		
Matches 132;	Conservative 74;	Mismatches 161;	Indels 74;	Gaps 15;
Qy	389	AMNSTOFLGSGVAVFSSGGDRIALQTLEOMIDCKYKLYGYDTOLDNLWLN--TEOWI	446	
Db	15	AIDNSSFOGLTGKVKFAN-NERGLVLDIKQNSDGVYFVAYDGDADFEKIIDSTKGM- 72		
Qy	447	GKYPQDFTIYTVLRTVLSLFLVCMCTISSCGYFVAFALIIFNWNKRRVIOSSHPVC	506	
Db	73	--SPPLDSTITERREHISLFLAM-----SLF-----IKSSPNL	107	
Qy	507	NTIMLFGVICLSVILIGIDGRFVSPEYPKICQARAWLIGTGFTLAYGAMFSKVRVH	566	
Db	108	NNIIIGSICFASVIMLGLDTRIVSDVFMVLCTYKTKTLCIGTSLFSFGAMFSKTVRH	167	

Qy	567	RFTTKAKDPKKKVPWKLYTMVSGSLSDILVLLSNQIFDPDQRLQRYLETFPLEDPVSTTD	626
Db	568	SIPTNIRMD-RKAIKDSKLFIIILGILLFIDICVLVMTWAFVSPFS-YTVT---	ELPHIPED
Qy	627	DIKTRPELEHCESORNWMLGLVYGFKGLLIVFGLFLAYETRSIKYKQINDSRYVCMSTY	686
Db	628	NIIVLPEVEKCNSSHGVSQAVLYAVKGVLMILGCLFLAMETRHVNVPALNDSKYIGTR--	687
Qy	687	NVVVLCILITAPVGMVIAQSDQASFAFVALAVIFCCFL--SMLLIFVPKVIIEIRHPDK	743
Db	688	-----TGQRDVQSRFV-----FCHLDDTNNVSRCAKDSFKSTPNFI	744
Qy	744	AESKYNPDASAISKEDE---ERYOKLYTENSQOLQRLITQKEEKIRIVLQRLVERGDAGTGE	800
Db	745	-----FSKNSYGGFNFKLSFGGFENIVFARSOVKKKVIELARNPV-----	801
Qy	801	LNG-ATGVASAAVATTSQPAS	820
Db	802	PRAYRGLMKSVVAKTSQPMSS	821
RESULT	3		
JH0563		metabotropic glutamate receptor 4 precursor - rat	
C:Species:		Rattus norvegicus (Norway rat)	
C:Date:		30-Jun-1992	#sequence_revision 30-Jun-1992
C:Accession:		JH0563; I58149	#text_change 17-Nov-2000
R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.			
Neuron 8, 169-179, 1992			
A:Title:		A family of metabotropic glutamate receptors.	
A:Reference number:		JH0561; MUID:92110002	
A:Accession:		JH0563	
A:Molecule type:		mRNA	
A:Residues:		1-912	<TAN>
R:O'Hara, P.J.; Sheppard, P.O.; Thogersen, H.; Venezuela, D.; Haldeman, B.A.			
Neuron 11, 41-52, 1993			
A:Title:		The ligand-binding domain in metabotropic glutamate receptors is	
A:Reference number:		I58149; MUID:93332699	
A:Accession:		I58149	
A>Status:		preliminary; translated from GB/EMBL/DBJ	
A:Molecule type:		mRNA	
A:Residues:		1-123,'R',125-912	<RES>
A:Cross-references:		GB:M90518; NID:g205400; PIDN:AAA93190.1; PID:g205401	
C:Comment:		This protein is coupled to a G protein and evokes a variety of	
C:Genetics:			

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Query Match      8.2%; Score 356.5; DB 2; Length 912;
Best Local Similarity 18.9%; Pred. No. 2.5e-19;
Matches 177; Conservative 164; Mismatches 374; Indels 221; Gaps 36;

Qy      5 WTSDGAVTFW--IFLLCLIAS-----PHLOGVGAGRP-----DELHTGGIPIAGK 48
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Db      1 MSGKGGAWWARLPLCLLLSYAPWPSSLGKRGHPHMNSIRIDGDTLGGGLFPVHGR 60
      49 GCGWQGOAC-----MPATRLALDDVKNQNPILLPGFKL----- 80
      : : : : : - : : : : : | | | | : | | | | : | |

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[illegible][illegible]

RESULT 4
I49142
metabotropic glutamate receptor 8 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: I49142
R:Duvoisin, R.M.; Zhang, C.; Ramonell, K.
J. Neurosci. 15, 3075-3083, 1995
A:Title: A novel metabotropic glutamate receptor expressed in the retina and olfactory bulb
A:Reference number: I49142; MUID:95239344
A:Accession: I49142
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-908 <RES>

Db 870 IQGNDR-----PGEVK-SEL-----CESLETNTSSTKTYTYSYSDHS 907

RESULT 5

A49874

metabotropic glutamate receptor 7 - rat

N:Alternate names: metabotropic glutamate receptor mGluR7

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999

C:Accession: A49874; I57954

J:Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R.; Mizuno, N.; Nakanishi, R. Biol. Chem. 269, 1231-1236, 1994

A:Title: Molecular characterization of a new metabotropic glutamate receptor mGluR7 comp

A:Reference number: A49874; MUID:94117433

A:Accession: A49874

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-915 <RES>

A:Cross-references: GB:D16817; NID:9458728; PIDN:BAA04092.1; PID:g458729

R:Saugstad, J.A.; Kinzie, J.M.; Mulvihill, E.R.; Segerson, T.P.; Westbrook, G.L.

Mol. Pharmacol. 45, 367-372, 1994

A:Title: Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric acid

A:Reference number: I57954; MUID:94195260

A:Accession: I57954

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-915 <RE2>

A:Cross-references: EMBL:U06832; NID:g459657; PIDN:AAA20655.1; PID:g459658

C:Genetics:

A:Gene: MGLUR7

C:Superfamily: metabotropic glutamate receptor 4

C:Keywords: neurotransmitter receptor

Query Match 8.1%; Score 353; DB 2; Length 915;

Best Local Similarity 21.2%; Pred. No. 4.8e-19;

Matches 206; Conservative 156; Mismatches 320; Indels 290; Gaps 50;

QY 17 LLCLIA-----SPH---LOGGVAGRPDELHIGGIFFIAGKGGWGGQAC----- 57

Db 24 LLCVLAARAGQEMYPHSHIRIEGDT-----LGGFLFPVHAKG--PSGVPCGDIKREN 74

QY 58 ----MPATRLALDDVNKQNPGLPGFKL---IL-----HNSDS 87

Db 75 GHRLEAMLYALDQINSDPNLLPNVTILGARILDTCSRDTYALEQSLTFVQALIQKDTSDV 134

QY 88 ECEPGLGASVMNLYNKKPKMLLAGC--STVCTTVAEAAKWNLVLCYGASSPALSD 145

Db 135 RCTNGEPP-----VFVKPEKVVGVIGAGSSVSMVANILRLFPQIPQISYASTAPELSD 188

QY 146 RKRFPFLRTHPSATVHNPTRIKMKFGWSRVAILQQAEEVFISTVEDLENRCMEAGVE 205

Db 189 DRYDFFSRVPPDSFQAQAMVDIVKALGN-----YVSTLAS-EGSGVGEKGE 236

QY 206 IVTRQSFSLDPTDAVNLR-----RQDA-----RIIVGLFVYVARRVLC-----EMYKOQL 252

Db 237 SFTQISKEAGGLCAQSVRIPOQRKORTIDFDRIIKOLLDTNPSRAVVFANDEDIKQIL 296

QY 253 YG--RA-HVWFFIGWYEDNW-----YEYNLKAEGITCTVEQMRIAAG--HLTTEAL 299

Db 297 AAKRADQVGHFLWVGSDSGMGSINLPHQHEDIAEG-AITIQPKRAVVEGFDAYFTSRTL 355

QY 300 -----MW-----NONNOTTISGMTAEF-RHRLNOLITEGYDINHDPYEGYOEAP 345

Db 356 ENNRNWNWAEYEEFNCKLTISGSKKEDTRKCTQGERI--GKDSNYEQ--EG--KVQ 409

QY 346 LAYDAVMSVALAFNPKTWERTLT-----GKSLRDFTYTDKTEADEIYAAMNS 392

Db 410 FVIDAVYAMAHALHNMKDLCADYRGVCPMEQAGGKKLKYIRHN----- 456

QY 393 TOFLGVSGV-VAFSSOGDRALQIQEOMIDGKYEKLGYYDTOLDNLW-----L 440

Db 457 --FNGSAGTPVFNKNGD-----APGRYDIFQYQTTNTNPGYRLIGOWTDELQ 504

QY 441 NTE--QWITGG--KVPQ-----VSLPLFVCMCTISSCGIFVAFALIININKHRR 459

Db 505 NIEDMQMGKGVREIPSSVCTLPCKPQRKKTOKGTPCCWTCPCDGYQYQFDEMTQCQHP 564

QY 460 -----VLR-----VLR-----VLR-----VLR-----VLR----- 564

Db 565 YDQRPENRTGCQNIPIIKLEWHSPWAVIPVFLMGLGIAT-IFVMAIFIRYN----DTP 619

QY 498 VIOSSHPVCNTIMLFGVITICILSVLLGIDGRFVSPEEYKPCICQARAWLLSTGFTLAYGA 557

Db 620 IVRASGRELVSLLTGIFLCYIITFLM-----IAKPD--VAVCSFRFVLGCMCISTAA 672

QY 558 MFSKVMRVHRETTAK---TDPKKKVEPWKLYTVMSGLSIDLVLLSQIDFPLQRYLE 614

Db 673 LLTKTNRIYRIFEQGKSVTAP-RLISPTSQLATSSLSISVQLLGVFWFGVDPPNIIID 731

QY 615 TFPLEDVSTDDKIRPELEHCEQSQRNMGLGVYKGLILVFLGLFLAYETRSIKVKQ 674

Db 732 ----YDEHKTNPQEQARGVLK-CDITDLQIICSL--GYSILLMVTCTVVAIKTRGVP-EN 783

QY 675 INDSRYGMSIYNVVVLGLITAPVGMVITASQODASFAFV-----ALAVIFCCFLSMLLIF 729

Db 784 FNEAKPIGFTMTTCIVWLAFIPI--FFGTAQSAEKLYIQTTLTISMNLSASVALGMLY 841

QY 730 VPKVIEVIRHPKDKAESKYNPDLSAISKEDERYKQLVTENEQORLITQKEEKIRVLQR 789

Db 842 MPKVYIIIFHPELNVQKR-----KRSEKAVVTAATMSSRLSHKPSDR----- 883

QY 790 LVERGDAGKTEL 801

Db 884 --PNGEAK--TEL 892

RESULT 6

JC7160

metabotropic glutamate receptor subtype 3 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000

C:Accession: JC7160

R:Minoshima, T.; Nakanishi, S.

J. Biochem. 126, 889-896, 1999

A:Title: Structural organization of the mouse metabotropic glutamate receptor subtype

A:Reference number: JC7160; MUID:20012997

A:Accession: JC7160

A:Molecule type: DNA

A:Residues: 1-879 <MIN>

A:Cross-references: GB:AF170696

C:Genetics:

A:Gene: mGluR3

C:Superfamily: metabotropic glutamate receptor 4

C:Keywords: differentiation; G protein-coupled receptor; receptor; transmembrane prot

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-879/Product: metabotropic glutamate receptor subtype 3 #status predicted <TM1>

F:577-599/Domain: transmembrane #status predicted <TM2>

F:614-634/Domain: transmembrane #status predicted <TM3>

F:646-664/Domain: transmembrane #status predicted <TM4>

F:689-709/Domain: transmembrane #status predicted <TM5>

F:735-756/Domain: transmembrane #status predicted <TM6>

F:770-791/Domain: transmembrane #status predicted <TM7>

F:804-828/Domain: transmembrane #status predicted <TM7>

Query Match 7.8%; Score 342; DB 2; Length 879;

Best Local Similarity 20.5%; Pred. No. 3.2e-18;

Matches 182; Conservative 132; Mismatches 300; Indels 272; Gaps 41;

QY 36 ELHIGGIFPIAGKGGWGGQAC-----MPATRLALDDVNKQNPGLPGFKILHS 84

Db 38 DLVLGGLFPINEKG--TGTEECRGINEDRGIORLEAMFLFAIDENKINKNLLYFGVLGVHI 95

QY 85 NDS-----ECEPGLGASVMNLYNKKPKMLLAGC--- 115

C:Accession: JH0562
R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A:Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:92110002
A:Accession: JH0562
A:Molecule type: mRNA
A:Residues: 1-879 <TAN>

A:Experimental source: brain
A:Comment: This protein is coupled to a G protein and evokes a variety of functions by a
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-879/Product: metabotropic glutamate receptor 3 #status predicted <MET>
F:577-599/Domain: transmembrane #status predicted <TRI>
F:614-634/Domain: transmembrane #status predicted <TII>
F:646-664/Domain: transmembrane #status predicted <III>
F:689-709/Domain: transmembrane #status predicted <TIV>
F:735-756/Domain: transmembrane #status predicted <TRV>
F:770-791/Domain: transmembrane #status predicted <TVI>
F:804-828/Domain: transmembrane #status predicted <VII>
F:209,292,414,439/Binding site: carboxyhydrate (Asn) (covalent) #status predicted
F:610,845/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 7.6%; Score 333; DB 2; Length 879;
Best Local Similarity 20.6%; Pred. No. 1.6e-17;
Matches 180; Conservative 132; Mismatches 313; Indels 250; Gaps 39;

Qy 36 ELHIGGIEPAGKGGWGGQAC-----MPATRLALDDVKNOPNLLPGFKLILHS 84
Db 38 DLVLGLFPINEKG--TGTEECGRINEDRGIQRLAIFAIDEINKDNYLLPGVKLGVIH 95
Qy 85 NDS-----ECPGLGASVYNNLLYKPKOKMLLAGC-- 115
Db 96 LDTCSRDTVALEOSLEFVRASLTQVDAEYKCPDG-----SYAQENIP---LIIAGVIG 147
Qy 116 ----STVCTTVAEAKMNNLIVLYGASSPALSDRKRPPTLFTHPSTVATVHNPTRIKMLKK 172
Db 148 GSYSSYSIQVANNLLRFQIPQISYASTSAKLSDKSRDYDFARTVPPDFYQAKAMAEILRF 207
Qy 173 FGHSRVAILQQAEEVISTVEDLE-----NRCMEAGVEIVTROSFLSDPTDAVRN-LRR 225
Db 208 FNNYTVSTVASEGDYGETGTEAEFEQEARLNICIT-ATAEKGVRNSIRKSYDSVIRELLQK 266
Qy 226 QDARIIVGLF-----YVVAARRVLCEMYKQOLYGRAHWFFIGYEDNNWYEVNKLAE 277
Db 267 PNARVV-LPMRSDDSRELIAANRV-----NASFTWV-----ASDGWG-----AQE 307
Qy 278 GITCTVQMRIRAAEGHLLTTEAL-----MNQNNQNTTIS 310
Db 308 SI---VKGSEHVAYGAITLLEASHPVRFQDRYFQSLNPNYNNHNPWFDRFEQFQCSLQ 364
Qy 311 GMTAEFRHLNQAALTEEGVDINHDPYEGYQEAPLAY--DAVWSVALAFNKTWERLTG 368
Db 365 -----NKRHHQVCDKHLAIDSSNYE---QESKIMFVYNAVYAMAHALKMORTLCPN 414
Qy 369 KKSRLDF--TYTDEKETADEIYAAMNSTOFL---GVSGVVAFFSSQGDRIALTOI--EQMI 420
Db 415 TYKLCDAKMLDKGKLYKEYLLKINFTAPNPNKGADSIKVFDFGDMGRYVNFNLOOT 474
Qy 421 DGKYY--KLGY---DTQLDNLWS-----LNTQE-----WI----- 446
Db 475 GGYSLVKVGHMAETLSLDVDSIHWRSNVSPTSCSDPCAPNEMKNQPGDVCWCICIPC 534
Qy 447 -----GGKVP-----QDRTIVTHVLRTVSLPLFCVCMC 473
Db 535 EPEYLVDEFTCMDCGPGOWPTADLSGCYNLPEDYIKWEDAWAIGPV--TIACLGFLCTC 592
Qy 474 TISSCGIFVAFALIFNWNKRR--VIOSSHPCVNTIMLFGVILICLISVILLAGIDGRF 530
Db 593 -----IVITVFIKHNNTPLVKASGRELC-YILLFGVSLSYCMTF-----F 631

Qy 531 VSPPEYPKICQARAWLLSTGFTLAYGAMFSKVMVRVHRETTAKTDPK--KKVEPKLYTM 588
Db 632 FIAKPSPVICALRLGLGTSAICYALLTNTCTARTIDGVKNGAQRPKFTSPSSQVFI 691
Qy 589 VSGLLSIDLVILLSWQIFDP--LQRYLETFFLEDDPVSTDDIKIRPELEHCSCSQSNMML 646
Db 692 CLGLILVQIVMVSWWLILETPTTRY--TLP-----EKRETVILKCNVKQSSMLI 739
Qy 647 GLVYGFKGLILVFLGLFLAYETRSIKVKQINDSRVYVGMISYNNVVLCLITAPVGMVIAQ 706
Db 740 SLTYDV--VLVILCTVYAFKTRKCP-ENFNEAKFIGFTMYTTCIIWLAFILFYFTSSDY 796
Qy 707 DASFAVALAVIFCCFLSMLLIFVPKVIETVRHPK 741
Db 797 RVQTTMTCISVSLSGFVVGLCLFAPKVHIVLPQ 831

RESULT 9

JH0561
metabotropic glutamate receptor 2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998
C:Accession: JH0561
R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992

A:Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:92110002
A:Accession: JH0561

A:Molecule type: mRNA

A:Residues: 1-872 <TAN>

A:Experimental source: brain

A:Comment: This protein is coupled to a G protein and evokes a variety of functions b
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p

F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-872/Product: metabotropic glutamate receptor 2 #status predicted <MET>
F:568-590/Domain: transmembrane #status predicted <TRI>
F:605-625/Domain: transmembrane #status predicted <TII>
F:637-655/Domain: transmembrane #status predicted <III>
F:680-700/Domain: transmembrane #status predicted <TIV>
F:726-747/Domain: transmembrane #status predicted <TRV>
F:761-782/Domain: transmembrane #status predicted <TVI>
F:795-819/Domain: transmembrane #status predicted <VII>

F:203,286,338,402,547/Binding site: carboxyhydrate (Asn) (covalent) #status predicted
F:601,675,827,837,843/Binding site: phosphate (Ser) (covalent) #status predicted
F:833/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 7.3%; Score 318; DB 2; Length 872;
Best Local Similarity 19.7%; Pred. No. 2.4e-16;
Matches 181; Conservative 135; Mismatches 330; Indels 274; Gaps 38;

Qy 17 LLCLIASPHLQGVAGRP-----DELHIGGIPIAGKGGWGGQACMP----- 59
Db 4 LLGLFALLMLMGAVAEPAKKVLTLEGDVLGLPLPVHOKGG--PAEECPVNEHRIQ 61
Qy 60 --ATRLALDDVKNOPNLLPGFKLILHSNDS-----EC 89
Db 62 LEAMLFALDRINRDPHLLPGVRLGAHLILSDCKDTHALEQALDFVRASLSRGADGSRHIC 121
Qy 90 EPLGASVYNNLLYKPKOKMLLAG--CSTVCTTVAEAKMNNLIVLYGASSPALSDRK 147
Db 122 PDG-----SYATHSDAPTAVTGVIGSYSDVSIQVANNLLRFQIPQISYASTSAKLSDKS 176
Qy 148 RPTLFRTHPSATVINPTRIKLMKFGNSRVAIL-----QOAEVFTS 190
Db 177 RYDFARTVPPDFQAKAMAEILRFNFTVYSTVASEGDYGETGTEAEFELEARNICVA 236
Qy 191 TVEDLENRCMEAGVEIVTROSFLSDPTDAVRN--RRDARIIVGLFYVVAARRVLCV 248
Db 237 TSEKVGGRAMSRAAFEGVVR-ALLQKPSARVAVLFRSEDADEL-----LAATQRL----- 285
Qy 249 KOOLYGRAHWVPFIGWYEDNNWYEVNKLKABGITCTVEQMRIRAAEGHLLTTEALM----- 300

Db 286 -----NASFTW-----ASDQWAL-----ESVAGSER-----AAGATIELASYPISDFAS 329
Qy 301 -----WNONOTTISGMTAEFR-----HRLNQAALIEEGYDINHRYPEGYQE 343
Db 330 YFQSLDPWNSRNPWFREFWEERFCHSRQRDCAAHSLRAVPE-----QE 375
Qy 344 APLAY--DAVWSVALAFNKTMRLE-----TTGKKSLRDFTYTDK----- 380
Db 376 SKIMEFVNNAVYAMAHALHNHRAALCPNTHLCDAMPVANGRRLYKDFVLNVKFDAPRPA 435
Qy 381 ETADEIYAAMNSTQFLGVSVVAFSSQGDRIALTQTEQIDG-----KYEKLGYY----- 430
Db 436 DTDE-----VRFDRGOGIGRYNFTYLRAGSGRYRYOKVGTWAEGLT 479
Qy 431 -DTQDNLNLSWLNTQWIGGKVPQDR---TIVTHVLRVSLPLFVC---MC----- 473
Db 480 LDTSF--IPWASPS---AGPLPASRCSEPCQLQNEVKSQV--PGEVCCWLCIPCQPYEYRLD 533
Qy 474 --TISCGI-----FVAF-----ALIIFNINKNHR 496
Db 534 EPTCADCGLGPWPNASLTGCFELPQBYIRMGDAWAVGPVTIACLGALATLFLVLGVFVRHN 593
Qy 497 R--VIOSSHPVCNTIMLFVGIICLSVILLGIDGRFVSPPEEYKPKICOARAWLLSTGTLA 554
Db 594 ATPVVKASGRELCYILGGVFLCYCMTFV-----FIA-KPSTAVCTLRRLGLGTAFSVC 646
Qy 555 YGAMFSKVMVRHRTTKAKTDPKKK--VEPWKLYTWSVGLSIDLVLISWQIFDPLQRY 612
Db 647 YSALTKTNRIRARIEGGAREGAQRPFISPASQVACLALISQILLIWAVALVVEAPGTG 706
Qy 613 LETFPLEDPVSTDDIKIRPELEHGESQRNSMWGLVYFGKGLILVFLGLAYETRISKY 672
Db 707 KETAPERREVTL-----RCNHRDASMLGSLAYNV--LLIALCTLYAFKTRKCP- 753
Qy 673 KOINDSRVGMISYVNVVLCITAPVGMVIAQQODASFAFVALAVIFCCFLSMLLIFVPK 732
Db 754 ENFNEAKFIGFTMYTTCIIWLAFPIFYVTSDDRYQTTMCVSVLSGSLVGLCLFAPK 813
Qy 733 VIEVIRHPKDKAESKYNPDS 752
Db 814 LHIILFQPKNVVSHRAPTS 833.

RESULT 10
A42916
metabotropic glutamate receptor mGluR5 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A42916
R:Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
J. Biol. Chem. 267, 13361-13368, 1992
A:Title: Molecular characterization of a novel metabotropic glutamate receptor
A:Reference number: A42916; MUID:93317054
A:Accession: A42916
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1171 <ABE>
A:Cross-references: GB:D10891; NID:g220813; PIDN:BAA01711.1; PID:d1002186; PID:g220814
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBI:107749, NCBI:107750)
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 6.9%; Score 303.5; DB 2; Length 1171;
Best Local Similarity 19.9%; Pred. No. 5.1e-15;
Matches 203; Conservative 144; Mismatches 387; Indels 287; Gaps 43;

Qy 30 VAGRPDELHIGGIPI-----AGKGGWGGQACMPATRLALDDVYNKQNPLLP 76
Db 28 VAHMPGDIILGALFSVHHQPTVDKVERKCGAVREQYQIRVEAMLHTLERINSDPTLLP 87
Qy 77 GFKLILHSND-----SECEPGL-----GASVMYNLLYNKPQL 109

RESULT 11
S71376
glutamate receptor homolog - cherry salmon
C:Species: Oncorhynchus masou (cherry salmon)
C>Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 01-May-1998

Db 88 NITLGCETROSCWHSNAVALEOSIEFIRDSLISSEEEGLVRCVGDSS-----SFRSKPIVG 144
Qy 110 MLLAGCSVTCTVAEAAKMWNLIVLCYGASSPALSDKRFRPTLFRTHPSATVHNPTRIKL 169
Db 145 VIGPGSSVAIQVQNLQLFNIQIAYSATSMDLSDKTLFKYFMRVVPDQAQARAWDI 204
Qy 170 MKKFGWSVALQOAEVFI STVEDLENRCMEAGVEIVTROSFLSDPTD-----AVRNLR 224
Db 205 VKRYNWTYVSVAHTEGNYGESGMEAFKDSAKREGICIAHSYKIYSNAGEQSFDKLLKKLR 264
Qy 225 RQ--DARTIIVGLFYVAARRVLCEMYKOOLYGRAHWFFIGWYEDNW--YEV-----NL 274
Db 265 SHLPKARVAVCFCEGTVRGILMAMRRUGLAGE-----FLILGSDWADRDVDTDGYORE 319
Qy 275 KAEGITTCVEQ-----MRTAAEGHLTEAL--MWNQNNOTTISGMTAE--EFRHR 320
Db 320 AVGGITIKLOSPDKVDFDDYILKLRPEINLRNPWFQEFQHRFCRLGEGFAQENSKYNT 379
Qy 321 LNQAALIEEGYDINHRYPEGYOEAPLAY--DAVWSVALAFNKTMRLETTGKKSRLDFTYT 378
Db 380 CNSSLTLRTHV-----QDSKMGFVINALYSMAYGLHNMQMSLCPGVAGLCD---A 427
Qy 379 DKEI-ADIEIYAAMNSTQFLGVSG--VFAESSQGDRIALTQIEOMIDGKYEKLYDYDTOLDN 436
Db 428 MKPIDGRKLLDSLMTNFTGVSQDMILFDENGDS-----PGRYEIMNFKEMGKDY 477
Qy 437 LSWLNTQEWIGGKVPQDRITV---THVLRV-SLPL----- 468
Db 478 FDYINVSQWNGELKMDDEDEWSKNNIIRSVCEPCEKQIKVIRKGEVSCCWTCTPCK 537
Qy 469 -----FVC-MCTISS-----CGIF-----VAFAL 486
Db 538 ENEVFEDEYTCACQQLGSWPTDDLTPQYLWGDPEPIAAVVFACGLGLATLFTV 597
Qy 487 IIFNWNKRRVIOSSHPVCNTIMLFVII-----CLISVILLGIDGRFVSPPEYKIC 540
Db 598 VIFTIYRDTVPVKSRSREL-C-YIILAGICLGLYCTFCLIA-----KPK-- 639
Qy 541 QARAWLLSTGF---TLAYGAMFSKVMVRHRTTKAKTDPKKKVPEWPKLYTMVSGLLSID 596
Db 640 QIYCYLQIRIGLSPAMSYSAVTKNRIARILAGS-----KKKCTKPRFMSACAQLVI 695
Qy 597 LVILLSQIFDPLQRYLETFPLEDPVSTDDIKIRPELEHGESQRNSMWGLV--YGFKG 654
Db 696 AFILICIQ---LGIIVALFIMEPPDMDHYPSIREVYLIC-----NTNLGVVTPLGNG 747
Qy 655 LILVFLGLAYETRISKVKQINDSRVGMISYVNVVLCITAPVGMVIAQQODASFAFVA 714
Db 748 LLILSCTFYAFKTRNVPA-NFNEAKYIAFTMYTTCIIWLAEVPI-----YFGSN 795
Qy 715 LAVIFCCF-----LSMLLIFVPEVIEVIRHPKDKAESKYNPDSAI-----SKEDE 759
Db 796 YKIITMCFVSLSATFVALGCMFVKVYIILAKPERNVRSAFTTSTVVRMHVGDGKSSAA 855
Qy 760 ERYOKLV-----TENEQ-----LQRL-----ITOKEK----- 782
Db 856 SRSSSLVNLKRRSGSGTSLSSNCKSVTWAQNEKSTROHLWQRLSVHINKENPNQFV 915
Qy 783 IRVLRQRLVERGD---AKGTENLGATGVASAAVATTSTOPASLINSSAHATPAATLAIQOG 839
Db 916 IKPPPKSTENRGPAAAGGGGPGVAGNAGCTATGgp-----EPPDAGPKALYDVAEA 970
Qy 840 E 840
Db 971 E 971

C:Accession: S71376
R:Kubokawa, K.; Miyashita, T.; Nagasawa, H.; Kubo, Y.
FEBS Lett. 392, 71-76, 1996
A:Title: Cloning and characterization of a bifunctional metabotropic receptor activated
A:Reference number: S71376; MUID:96354880
A:Accession: S71376
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1218 <KUB>
C:Keywords: glycoprotein; phosphoprotein
F:603-625/Domain: transmembrane #status predicted <TM1>
F:640-660/Domain: transmembrane #status predicted <TM2>
F:672-690/Domain: transmembrane #status predicted <TM3>
F:717-737/Domain: transmembrane #status predicted <TM4>
F:761-782/Domain: transmembrane #status predicted <TM5>
F:796-817/Domain: transmembrane #status predicted <TM6>
F:826-850/Domain: transmembrane #status predicted <TM7>
F:104,233,403,525,757/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:636,699,961/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status pre
F:705/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:892/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predic

Query Match 6.9%; Score 303; DB 2; Length 1218;
Best Local Similarity 19.5%; Pred. No. 5.9e-15;
Matches 173; Conservative 144; Mismatches 346; Indels 222; Gaps 35;

QY 30 VAGRPDELHIGGIPPI-----AGKGWGGQACMPATRLALDDVKNQPNLLP 76
DB 44 VARMDGDIIGALFVSHVHQPTQVAERKCGEVREYQIGRVEAMPHPTLDRLNSNENLLP 103
QY 77 GFKLILHNSDS--ECEPGIGASVMY-----NLL-----YN 104
DB 104 NITLCEIRDSCHWSVALEQIEFIRDSLSIRDDNDKGTSRQWCEGMPPSQPATK 163
QY 105 KPQKMLLAGCTVCTTVAEAAKMNLIIVLCYGASSPALSDRKRFTLFRTHPSATVHPN 164
DB 164 RPIAGVIGGSSVAIQVONLQLNIPQIAYSATSIDLSKTLFKYFLRVVPSDTLQAR 223
QY 165 TRIKMKFGWGRVAILQAAEEVISTVEDLENRCMEAGVEIVTQSFSLSDPTD-----A 219
DB 224 AILDIVKRYNTWTVSAVHTEGNYGSGMEAPFELASQELGCTAHSDKIYSNAGEKHFDRL 283
QY 220 VNNLRQ--DARIIVGLFVVAARRVLCYKQOOLYGRAHVFFIGWEDNW----- 269
DB 284 LRKLRPLPKARVVCFCGEMTVRGLLMARR---LGVAGEFLIG--SDGWADRDVEVE 338
QY 270 -YE-----VNLKAEGITCTVE---QMRIAEGHLLTEALMNQNNQTTISGMTAEF 317
DB 339 GYEQSAVGGITVKLHSEEVTSFDDYFLKRLNTNTRNPFPEFWQHRFQCRIPGHPLENN 398
QY 318 RHRLNQAALIEGYDINHRYPEGYQAPLAY--DAVMSVALAFNKTWERLTTCGKSLRDF 375
DB 399 NYRKNCS---GYESLEDNY---VQDSKMGFVINAIYMAAQLHDSHSLCPGHVGL--C 449
QY 376 TYTDKEIADEIYAAMNSTOFLGVSGV-VAFSSQGDRIALTQIBQMDIGKYELGYDTQL 434
DB 450 KAMPIDGSGOLLEFLMRTSFTGSGEDVWFDENGD-----TPGRVEINNLYQVEP 499
QY 435 DNLWNLTEOWIGGKVPQDRTIV-----THVLRTVSLP-----LFCV-- 471
DB 500 GAFDIYNGVSWHEGQLSIDDYMMQINRSDMLVSCVSEPCSKGEIKVIRKEVSCCWICTA 559
QY 472 -----MCT-----ISSC-GIFV-AF 484
DB 560 KCDNEIVQDEFTCTACDLGWFPDPELEGCEPTILRYLENGNPNESIVQVVFACILGILTSF 619
QY 485 ALIIFNWNKRRVIOSSHVPCNTIM--LFGVILICILSVILLGIDGRFVSPEEYPKI--C 540
DB 620 VTFIEVLYRDPVWKSRRRELVCYIILAGIFLGYICPFTLI-----AQPVTASC 667
QY 541 QARAMLLSTGFTLAYGAMFSKVRVHRFTTKAK-----TDPKKVPEWPKLWTMVGSLISD 596

DB 668 YLQRLVLGLSATWCYSALVTKTNRIARILAGSKKKICTRKPRESMAWAQLVIAGLLVSQ 727
QY 597 LVILLWSQIFDPQRYLETPELDVPTDDDIKTRPELEHCESSORNSWMLGLV--YGFKG 654
DB 728 LTLVEFTLILLEP-----PM-----PVKSPYSIREVFLICNTSTVGWVAPLGYNG 771
QY 655 LILVFGFLAYETRSIKVKOINDSRYVGMSTIYNVVLCLITAPVGM-----VIASQODAS 709
DB 772 LLIMSCYYAFKTRNVA--NFNEAKYIAFTWYTCIIWLAPVPIYFGSNYKLIIT---S 826
QY 710 FAFVALAVIFCCFLSMILLIHPKVIIEHRPKDKAESKYNPDSAI 754
DB 827 FS-VLSVT-----VALGCMFSPKIYIILAKPERNVRSAFTSDVY 866

RESULT 12
JC2132
metabotropic glutamate receptor 5 A - human
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
C:Accession: JC2132
R:Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
A:Title: Molecular cloning and the functional expression of two isoforms of human met
A:Reference number: JC2131; MUID:94197696
A:Accession: JC2132
A:Molecule type: mRNA
A:Residues: 1-1180 <MIN>
C:Comment: This protein is coupled to guanine nucleotide binding proteins.
C:Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein
F:360-604/Domain: transmembrane #status predicted <TM1>
F:617-637/Domain: transmembrane #status predicted <TM2>
F:644-664/Domain: transmembrane #status predicted <TM3>
F:694-714/Domain: transmembrane #status predicted <TM4>
F:738-759/Domain: transmembrane #status predicted <TM5>
F:773-794/Domain: transmembrane #status predicted <TM6>
F:803-827/Domain: transmembrane #status predicted <TM7>

Query Match 6.9%; Score 302.5; DB 2; Length 1180;
Best Local Similarity 20.1%; Pred. No. 6.1e-15;
Matches 208; Conservative 141; Mismatches 375; Indels 311; Gaps 44;

QY 30 VAGRPDELHIGGIPPI-----AGKGWGGQACMPATRLALDDVKNQPNLLP 76
DB 28 VAHMPGDIIGALFVSHVHQPTQVHKVRCGAVREYQIGRVEAMLHTLERINSPTLLP 87
QY 77 GFKLILHNSD-----SECEPL-----CASVMYNNLYNKPQKL 109
DB 88 NITLCEIRDSCHWSVALEQIEFIRDSLSISEEEGLVRCVDSGSSSFR--SKKPIVG 145
QY 110 MLLAGCTVCTTVAEAAKMNLIIVLCYGASSPALSDRKRFTLFRTHPSATVHPNTRIKL 169
DB 146 VIGGSSVAIQVONLQLNIPQIAYSATSMDSKTLFKYFMRVVPSSDAQQAAMVDI 205
QY 170 MKFGWGRVAILQAAEEVISTVEDLENRCMEAGVEIVTQSFSLSDPTD-----AVRNL 224
DB 206 VKRYNWTVVSAVHTEGNYGSGMEAFKDSAKEGICIAHSYKIYSNAGEQSFDKLLKLT 265
QY 225 RQ--DARIIVGLFVVAARRVLCYKQOOLYGRAHVFFIGWEDNW---YEV-----NL 274
DB 266 SHLPKARVAVCFCEGTVRGLLMARRLGLAGE-----FLLGSDGWADRDVDTQGYRE 320
QY 275 KAEGITCTVEQ-----MRTAAEGHLLTEALMNQNNQTTISGMTAEFRHRLNQA 324
DB 321 AVGITIKLQSPDVKNWFDYILKLRPE---TNHRNPFQ-----EFWQHRFOCR 366
QY 325 LIEEGYDINHRY-----PEGYQAPLAY--DAVMSVALAFNKTWERLTGKGS 371
DB 367 L--EGFPOENSKYKNTCNSSLTLKTHVQDSKMGFVINAIYSMAVGLHNMOMSLCPGYAG 424
QY 372 LRDTTYTDKEI--ADEIYAAMNSTOFLGVSG--VFAFSSQGDRIALTQIBQMDIGKYEKLYG 429


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Db      817 WRH--HYPTTRDQVVLT-----CNPDPDHHFLYSLAY--DGFLLVLCCTTYAVKTRK 861
Qy      670 IKVKQINDSRVGVGSIYNNVVLCILITAPGVGMVITASQODASFAPVALAVIFCCFLMLLIF 729
Db      862 VP-ENFNETKFIGFSMTTCVVNLWSWIFFFGTSGDFOIQTSSLCISISMSANVALACIF 920
Qy      730 VPK--VIEVIRHP---KDKAESKYNPDS-----AISKEDEERYOKLVTENEQIQ 773
Db      921 SPKLWILLFEKHKKNVRQEGESMLNKSSRLGNCSSRLCANSIDEPNOYTALLTDSTR-- 978
Qy      774 RLITQKEEKIRVLQRILVERGDAGKTELNGATGVASAAVATTSPQASLINSSAHAT 829
Db      979 -----RRSSRK-----TSQPTS--TSSAHD 997

RESULT 15
A41939
G protein-coupled glutamate receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1994
C:Accession: A41939; S15362
R:Houamed, K.M.; Kuiper, J.L.; Gilbert, T.L.; Haldeman, B.A.; O'Hara, P.J.
A:Title: Cloning, expression, and gene structure of a G protein-coupled gl
Science 252, 1318-1321, 1991
A:Reference number: A41939; MUID:92022526
A:Accession: A41939
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-1199 <HOU>
A:Cross-references: GB:M61099; NID:g397806; PIDN:AAA19497.1; PID:g204460
A:Experimental source: cerebellum
A:Note: sequence extracted from NCBI backbone (NCBIP:60785)
R:Masu, M.; Tanabe, Y.; Tsuchida, K.; Shibamoto, R.; Nakanishi, S.
Nature 349, 760-765, 1991
A:Title: Sequence and expression of a metabotropic glutamate receptor.
A:Reference number: S15362; MUID:91156047
A:Accession: S15362
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1199 <MAS>
A:Cross-references: EMBL:X57569; NID:g56646; PIDN:CAA40799.1; PID:g56647
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match          6.1%   Score 268:   DB 2:   Length 1199;
Best Local Similarity 18.8%; Pred. No. 3.1e-12;
Matches 168; Conservative 146; Mismatches 354; Indels 228; Gaps

Qy      20 LIASPHLQGGVAGRPDELHIGIETPI-----AGKGWGGQGCAMPATRLALD 66
Db      28 LLGASSQSVARMWDGVIIGALFSVHHQPPAEKVPKCKGEIREQYGIQVRVMEFTLD 87
Qy      67 DVNKQPNLLPGFKLILSNDG--ECPEGLGASVMY----NLL----- 102
Db      88 KINADPVLLPNITLTGSEIRDSCHWSSVALEQSIETFIKSLISIRDEXDKGLNRLCPDGQTL 147
Qy      103 ---YINKPKLMLLAGCGTCTTVAEAKMWNLLVLCYGASSPALSDRKREPTLFTHPS 158
Db      148 PPGRTKPKIAGVIGPGSSVAIQVONLLQFLDIPQIAYSATSIDLSOKTLYKFLRVVPS 207
Qy      159 ATVINPTRIKMLKFGSRVAILOQAQAEVETISVEDLENRCMEAGVIVTRQSFSLDPTD 218
Db      208 DTLOARMLDIVKRYNWTIYVSAVHTGNYGESGNDAPFELAAQEGLCIAHSDKIYSNAGE 267
Qy      219 -----AVENLRQ---DARIIVGLFVYVAARVLCENYKQOYLGRAHWVFFIGWYEDN --- 268
Db      268 KSFDRLRLKRLRPLKARVVVCFCEGTVRGILLSAMRRLGVGVGEFSLIGSDGNADRDEVI 327
Qy      269 -WYEVNLIKAEGITCTVEQMRITAA-----EGHLTTEAL-----MNQNNQTTISGMTAE 315
Db      328 EGYEVEANG-GITIKLAQSPVRSFDDYFLKRLDLDTNTPNPFPEFVQHRFCQLPGLHLE 386

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Qy	316	EFRHRL-----NOALIEBEGYDINHDRYPEGVQOERAPLAY--DAVWSVALAFNKMTWERLUTTKC	369
Db	387	NPNEFKVCTGNESL-EENY-----VQDSKMGFVINAIVAMAHLQNMHHALPCGH	435
Qy	370	KSLRDF--TYTDREIADEIYAAMNSTQFLGVSG-VVAFSSQGDRIALTQIEQWIDCKYKX	426
Db	436	VGLCDAMKPIDGRKLDDFLI-----KSFVGVSGEEVWFDEKGD-----APGRYDI	481
Qy	427	LGYDYDTQDLNLSWLNTBQWIGGKVPQD-----RTIVTH-----VLRTVSL	466
Db	482	MNLQYTEANRYDYVHVCTWHEGVNLTDYKIOMKSGMVRSCPELKGQIKVIRKGV	541
Qy	467	PL-----FVC-MCTIS-----SC	478
Db	542	SCCWICTACKENEFVQDEFTCRACDLGWPNAEILTCEPIPVRYLEWSDIESIIATFSC	601
Qy	479	-GIFVA-FALIIFNWNKHRRVTOSSHPVCNTIMLFGVIICLISVILLGIDGRFVSP---	533
Db	602	LGILVTLFVLILFVLYRDTPWAKSSSREL-----YIILAGIFLGYVCPFTL	648
Qy	534	--EYYPKICQARAWLLSTGFTLAYGAMFSKVMVRHRTTKAK---TDPKKVPEPKLTY	587
Db	649	IAKPTTSCYLQRLLVGLSSAMCYSALVTKTNRIARILAGSKKKICTRKPMSAWAQVI	708
Qy	588	MVSGLLSIDLVLLSMQIFDPLQRYLETFFLEDPVSTDDIKIRPELHCEGSORNSMWLG	647
Db	709	IASILISVQLTVLVTLIMEP-----PM-----PILSYPSIKEVYLICNTSNLG	752
Qy	648	LV--YGFKGHLIVFLGFLAYETRSIKVKQINDSRYYGMSIYNVVVLCILITAPVGMVIA	705
Db	753	VWAPVGYNGLLMSCTVYAFKTRNVPA-NFNEAKYIAFTMYTTCIIWLAFVPI-----	804
Qy	706	QDASFAPVALAVFCCPLSMILLI-----FVPKVIETVRHPKDKAESKYNPD	754
Db	805	-----YFGSNTKIITFCPAVLSVTVLALGCMFTPKMVIITIAKPERNVRSFTTSDV	856

Search completed: April 30, 2002, 10:13:34
Job time: 141 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:12:08 ; Search time 9.1 Seconds
(without alignments)
713.191 Million cell updates/sec

Title: US-09-715-962-2
Perfect score: 4374
Sequence: 1 MRKDWTSYGATFWIFLCL.....LINSSAHATPAATLAIQGE 840

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 46456 seqs, 7726236 residues

Total number of hits satisfying chosen parameters: 46456

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_New.*
1: /cgn2.6/ptodata/1/paa/PCT_NEW_COMB.pep.*
2: /cgn2.6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2.6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2.6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2.6/ptodata/1/paa/US09_NEW_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	359	8.2	908	1	PCT-US01-47325-3
2	358	8.2	915	1	PCT-US02-05625-67
3	355	8.1	915	1	PCT-US02-05625-8
4	355	8.1	915	1	PCT-US02-05625-71
5	354	8.1	915	1	PCT-US02-05625-69
6	350	8.0	915	1	PCT-US02-05625-73
7	222	5.1	858	6	US-10-035-045-14
8	205	4.7	839	6	US-10-035-045-21
9	190.5	4.4	852	6	US-10-035-045-4
10	180	4.1	841	6	US-10-035-045-17
11	108	2.5	403	1	PCT-US02-07826-121
12	108	2.5	403	6	US-10-097-340-121
13	104.5	2.4	911	1	PCT-US02-06415-6
14	104.5	2.4	911	1	PCT-US02-06415-8
15	103	2.4	498	5	US-09-540-209B-10405
16	103	2.4	498	1	PCT-US02-09944-663
17	102.5	2.3	728	6	US-10-036-492-5
18	100.5	2.3	253	5	US-09-540-209B-9343
19	98.5	2.3	199	5	US-09-975-553-18
20	95.5	2.2	1124	1	PCT-US02-03635-7
21	95.5	2.2	1440	5	US-09-573-655B-1303
22	94.5	2.2	716	6	US-10-036-492-11
23	94.5	2.2	762	7	US-60-370-796-25
24	94	2.1	199	5	US-09-975-553-2
25	93	2.1	262	5	US-09-540-209B-9117
26	92.5	2.1	197	5	US-09-975-553-8

ALIGNMENTS

RESULT 1
PCT-US01-47325-3
; Sequence 3, Application PC/TUS0147325
; GENERAL INFORMATION:
; APPLICANT: Genaissance Pharmaceuticals, Inc.
; APPLICANT: Bieglecki, Karyn
; APPLICANT: Chew, Anne
; APPLICANT: Choi, Julie Y.
; APPLICANT: Koshiy, Beena
; APPLICANT: Parks, Katie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE GRM8 GENE
; FILE REFERENCE: GRM8_MWH-1725PCT
; CURRENT APPLICATION NUMBER: PCT/US01/47325
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/247,576
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 908
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-47325-3

Query Match 8.2%; Score 359; DB 1; Length 908;
Best Local Similarity 21.1%; Pred. No. 1.1e-21;
Matches 204; Conservative 153; Mismatches 378; Indels 232; Gaps 44;
Qy 13 FWIFLCLIASPHLOGGVAG-RPD-ELHIGIFPIAGKGGWGGQAC-----MP 59
Db 22 YWI--LTMQRTSHQSEVAHSIRVDGDIILGLFPVHAKG--ERGVPCCGELKKERGIHRL 77
Qy 60 ATRLALDDVKNQPLLPGFKL---IL-----HNSDSECEPGL 93
Db 78 AMLYAIQDKNDPDLNLTGLVRILDFCSRDVTVALEOSLTFVQALIEKDSADVKCANGD 137
Qy 94 GASVYMLLYNKPQKL--MLLAGCSTVCTTVAEAKMNNLIVLCYGASSPALSQRKRPT 151
Db 138 PP-----IFTRPKISGVICAAASSVSIMVANTILRLEKIPQISYASTAPELSDNTRVDF 191
Qy 152 LFRTHPSATVHNPTRIKLMKFGWSRVAILQQAEEVFISTVEDLENROME-AGVEIVTRQ 210
Db 192 FSRVVPDSYQAQAMVDIVTALGNVYSTLASSENGYSGESVEAFQISREITGGVCIASQ 251
Qy 211 SFLSDPTDA-----VNLRRQDARIIVGLFYVVAARVLCENYKQQLYGRAHWFFIGW 264
Db 252 KIPREPRGPEFKTIKRLLETPNARVIMFANEDDIRLEAAKKLNQSGH---FLWIG- 307

QY 393 TOFLGSGV-VAFSSQGDRIALTOEQMIDGKYEKGLGYDTOLDNLW-----L 440
Db 455 VNFNGSAGTVMFNKNGD-----APGRYDIFQYQTTNTSNPGYRLIGQWTDLQL 504
QY 441 NTE--QWIGG--KVP----- 451
Db 505 NIEDMONGKGVREIPASVCTLPCKPQQRKTKGTPCCWTCPCDGYQYQFDEMTQCHP 564
QY 452 -----QDRTIVT---HVLRTVSLPLFVCMCTISSCGIFVAFALIIIFNWNKHR 496
Db 565 YDQRPENRTGCDIPIIKLEWHPWV-IPVFLAMLGIIAT-IFVMAFIRYN-----DT 618
QY 497 RVIOSSHPCVNTIMLFGVILICLSVLLGIDGRFVSPPEYPKICQARAWLLSTGFTLAYG 556
Db 619 PIVRASGRELSVLLTGIFLCYIITFLM-----IAKPD--VAVCSFRRVFLGLGMCISYA 671
QY 557 AMFSKVRVHRFTTKAK---TDPKKVPEWKLVTWVSGLLSIDLVLLSWQIFDPLQRYL 613
Db 672 ALLTKNRIYRIFEQGKKSVTAP-RLISPTSQAIATSSLSISVQLLGVFIFWGVDPNIII 730
QY 614 ETFFLEDVSTDDIKIRPELEHESQORNMMGLVYGFKGLILVFLGLFLAYETRSIKVK 673
Db 731 D-----YDEHKTMPNEQARGVLK-CDITDLQICSL--GYSILLMVTCVYAIKTRGVP-E 782
QY 674 QINDSRVGMISYNNVVVLGLITAPVGMVIAQQDASFAFV-----ALAVIFCCFLSMLLI 728
Db 783 NFNEAKPIGFTMYTTCIVWLAFIPI--FFGTAQSAEKLYIQTTLTISMNLSASVALGML 840
QY 729 FVPKVEIVRHPKDAESKYNPDSAISKDEERYQKLVTEQQLRLITQKEEKIRVLQ 788
Db 841 YMPKVYIIIFHPELNVQKR-----KRSFKAVVTAATMSSRLSHKPSDR----- 883
QY 789 RLVERGDAGKTEL 801
Db 884 ---PNGEAK-TEL 892

RESULT 5

PCT-US02-05625-69

; Sequence 69, Application PC/TUS0205625

; GENERAL INFORMATION:

; APPLICANT: Arena Pharmaceuticals, Inc.

; TITLE OF INVENTION: Endogenous And Non-Endogenous, Constitutively Activated G Protein

; FILE REFERENCE: AREN-0321

; CURRENT APPLICATION NUMBER: PCT/US02/05625

; CURRENT FILING DATE: 2002-02-26

; NUMBER OF SEQ ID NOS: 102

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 69

; LENGTH: 915

; TYPE: PRT

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Novel Sequence

PCT-US02-05625-69

Query Match

Best Local Similarity 8.1%; Score 354; DB 1; Length 915;

Matches 209; Conservative 153; Mismatches 319; Indels 292; Gaps 50;

QY 17 LCLCIA-----SPH---LOGGVAGRPDELHIGGIFPIAGKGWQGOAC----- 57
Db 24 LICALAAARGQEMVAPHISIRIGDVT-----LGLLFPVHAKG--PSGVPCGDIKREN 74
QY 58 ----MPATRALADVVKQNPALPGFKL---IL-----HSNDS 87
Db 75 GTHRLEAMLYALQINDPNLLPNVLGARILDTCSRDTYALEQSLTFVQALIQDTSV 134
QY 88 ECEPGLGASWYNNLYNKKOKMLLAGC---STVCTTVAAEAKMWNILVLCYGASSPALSD 145
Db 135 RCTNGEPP-----VFVKPEKVVGVIGASGSSVIMVANILRLFPQIPQISYASTAPELSD 188

ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Novel Sequence
PCT-US02-05625-73

Query Match 8.0%; Score 350; DB 1; Length 915;
Best Local Similarity 21.5%; Pred. No. 6.4e-21;
Matches 209; Conservative 152; Mismatches 320; Indels 292; Gaps 50;

Qy 17 LLCLIA-----SPH-----LOGGVAGRPDELHIGGIFPIAGKGGWGGQAC-----57
Db 24 LLCAAAAAGQEMAPHSTRIGEDYT-----LGLFPVHAKG--PSGVPCGDIKREN 74

Qy 58 ----MPATRLADVDVKNQNLPGFKL---IL-----HNSD 87
Db 75 GIHRLAEMYALDQINSDPNLNVTLGARILDTCSRDTYALQESLTFVQALIQKDTSDV 134

Qy 88 ECEPGLGASWYNLLYNKKOKMLLAGC--STVCTTVAEAAKWNLLVLCYGASSPALSD 145
Db 135 RCTNGEPP-----VFVKPEKVVGVIGASGSSVIMVANILRLFQIPQISYASTAPELSD 188

Qy 146 RKRFPFLRTHPSATVHNPTRIKMKKFGSRVAILQQAEEVFISTVEDLENRCMEAGVE 205
Db 189 DRYDFFSRVPPDSFOAQAMVDIVKALGN-----YVSTLAS-EGSGEKGVE 236

Qy 206 IVTROSFLSDPTDAVRLNR-----RODA-----RIIVGLFYVVAARRVLC-----EMYKOOL 252
Db 237 SFTQISKEAGGLCIAQSVRIPOERKDTIDFRIIKQLLDPNSRAVVIFANDEDIKOIL 296

Qy 253 YG--RA-HVWFFIGWEDNW-----YEVNKAEGITCTVEQMRIAAG---HLITTEAL 299
Db 297 AAARADQVGHFLVWGSDSWGSKINPLHQHEDIAEG-AITIQKRAIVVEGFDAYFTSRTL 355

Qy 300 -----MW-----NONNOTTISGMTAEF-RHRLNOALIEGYDINHRYPEGYOEP 345
Db 356 ENNRNVWAEWEEFNPKLTISSKKEDTDRKCTQGERI--GKDSNYEQ--EG--KVQ 409

Qy 346 LAYDAVMSVALAFNKMTMERLTT-----GKKSURDFTYTDKEADEIYAAMNS 392
Db 410 FVIDAVYAMAHALHHNKDKLCADYRGVCPMEQAGKKLLK-----YRN 454

Qy 393 TQPLGVSGV-VAFSSOGDRIALTOIEQMDGKYEKGLGYDTQDNLWS-----L 440
Db 455 VNFNGSAGTPVAFNKNGD-----APGRYDIFQYQTTNTSPNGYRLIGOWTDELQ 504

Qy 441 NTE--QWIGG--KVP-----IAKPD--VAVCSFRFVLGLGMCISYA 671
Db 505 NIEDQWQGVGREIPASVCTLPCKPGQRKKTQGTGCCWTCPCDGVQYQFDEMTQOHP 564

Qy 452 -----QDRITVT---HVLRTVSLPFCVMTISSCGIFVAFALIIENIWNKHR 496
Db 565 YDQRPENRTGCQDIPLIKLEWSPWAV-IPVFLAMLGIIAT-IFVMATIRYN-----DT 618

Qy 497 RVIQSHPVNCTIMLGVICILISVILLGIDGRFVSPEEYKPCQARAWLLSGTFLAYG 556
Db 619 PIVRAGRELSVLLTGIELCYITITFLM-----IAKPD--VAVCSFRFVLGLGMCISYA 671

Qy 557 AMFSKVRVHRTTKAK---TDPKKKVEPKLYTMVSGLLSIDLVILLSHQIDPLQRYL 613
Db 672 ALLTKNRIYRIFEQKSKSVTAP-RLISPTSQLAITSSLSVQLLGVFIWGVDPNNIII 730

Qy 614 ETFFLEDPVSTDDIKIRPELEHESQSNMGLVGVGKGLJLVFLFLAYETRSIKVK 673
Db 731 D-----YDEKTNWPEQARGVLK-CDITDQIICSL--GYSILLMVTCTVVAIKTRGVP-E 782

Qy 674 QINDSRVGMISYNNVVLCLITAPVGMVITASQODASFAFY-----ALAVIFCCFLSMLLI 728
Db 783 NFNEAKPKGFTMYTTCIVWLAFIPI--FEGTAQSAEKLYIQTTLTISMNLSASVALGML 840

Qy 729 FVPKVIETIRHPDKAESYNPDSAISKEDEERYQKLVTENEQORLITQKEKIRVLRQ 788
Db 841 YMPKVYIIIFHPDELNVQKR-----KRSFKAVVTAATMSSRLSHKPSDR-----883

Qy 789 RLVERGDAKGTTEL 801
Db 884 ---PNGEAK-TEL 892

RESULT 7
US-10-035-045-14
; Sequence 14, Application US/10035045
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: LI, XIAODONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: T1R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003-0280681
; CURRENT APPLICATION NUMBER: US/10/035,045
; CURRENT FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: 60/259,227
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 60/284,547
; PRIOR FILING DATE: 2001-04-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 14
; LENGTH: 858
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-035-045-14

Query Match 5.1%; Score 222; DB 6; Length 858;
Best Local Similarity 19.7%; Pred. No. 2e-10;
Matches 185; Conservative 129; Mismatches 324; Indels 302; Gaps 44;

Qy 18 LCLTASPHLOGGVAGRPDELHIGGIFPIAGKGGWGGQACMP-----A 60
Db 23 LCLSQQKAQG-----DYILGGLFPIGTTTEATLNQRTOPNGILCTRFSPGLFLAMA 75

Qy 61 TRLALDDVKNQNLPGFKLILHNSDSECP--GLGASVMY-----NLLYNK 105
Db 76 MKMAVEEINNGSALLPGRLGTYDLETCSEPVVTHKPSLMFAKVGSOSIAAYCNYTQY 135

Qy 106 PQKMLLAGCSTVCTTVAEAAKWNLLIVL---CYGASSPALSDRKRFPFLRTHPSATVH 162
Db 136 PRVLAVIGPHSSELALI--TGKFFSFFLMPQVSYSSASMDRLSDRETFEFPFTVPSDRVQ 193

Qy 163 NPTRIKMKKFGSRVAILQQAEEVFISTVEDLENRCMEAGVEIV-----TRQSFL 213
Db 194 LQAVVTLLQNFSWNVAAALGSDDDYRGREGLSIFSGLSANRSGICIAHEGLVPOHDTSGOOL 253

Qy 214 SDPTDAVNLRRQDARIIVGLFYVVAARRVLCEMYKQOLYGRAH-----VWFFIGWYEDN 268
Db 254 GKVDVLRQVNSQVQVYV-LF--ASARAV-----YSLFSYILHDLSPKVW-----297

Qy 269 WYEVNLAEGITCTVEQMRIAAGHLTTEALMWNQ--NQTITSGMTAE-----EFRHRL 321
Db 298 -----VASEWLTSDLVMTLPIARIARVGTIVLGLQGALLPFSHYV 338

Qy 322 NOAL-----IEE-----GYDINHRY 337
Db 339 ETRLAADPTFCASLKAELDEERVMPRCQCDYIMLQNLSSGLMQLNSAGOLHHQIF 398

Qy 338 PEGQOEAPLAYDAVMSVALAFNKT-----MERLTGKKSRLDFTY- 377
Db 399 -----ATYAAVYSVAQALHNTLQCNVSHCHTSEPQPMQLLENMYNMSFRADLTQL 450

Qy 378 -----TDKEADEIYAAMNSTQFLGVSQVAFSSQ-----GDRIALTOI-EQMD 421
Db 451 FDAKGSVDMEYDLKMWVWQSPPTPVLTHTVTNGTLQLOHKSVMYPCNQVPSVQCSRQCKD 510

Qy 422 GK-----YE-----KLGYDYTDQDNLWS--LNTQEWITGK-----VP-QDRTIVTH 459

Db 511 GQRRVKGPHSCCYDCVCKAGSYRKHDPDDFTCTPCGKDWSEKSTTCLPRPKFLAWG 570
Qy 460 VLRVSLPLFCM--CTISSCGIFVAFALIIFNINMKHRRVIQSSHPVQNTIMLFGVII 516
Db 571 EPVLSLLLLCLVLGLTLAALGLFVHY-----NDS--PLVQASG--GSLFCFG-LI 617
Qy 517 CL-----ISVILGIDGRFVSPPEYKICQARAWLLSTGFTLAYGAMFSKVRVHRFTTKA 572
Db 618 CLGLFCLSVLLFPGPRSRAS-----CLAAQPMHPLTGLCLSTLFLQAAIF----- 664
Qy 573 KTDPKKKE-----PWKLYTMVSGLLSDLVLLSQIFDPLQRYLET 615
Db 665 -----VESEPLSWANMLCSYLRGPWAWLVL--LATLVEAALCAW-----YLMA 707
Qy 616 FPLEDPVSTDDIKRPE--LEHCEQSNMGLGLVYGFGLILVFLGLFLAYETRSLKVK 673
Db 708 FPE-----VVTQWQLPTEVLEHCR--MRSWVSLGLVH--INNAVLAFLCLGTFELVQSQPG 761
Qy 674 QINDRYGMSIYNNVVLCLITAPVGMVIAQQDASFAFVALAVIFCCFLSMLLIF--VPK 732
Db 762 RYNRARGLTAFMLAYFIWVSFVP--LLANQVAVQPAVOMGAILFCALGILATPHLPK 818
Qy 733 VIEVI-----RHPKDKAESKNPDSAISKEDE 759
Db 819 CYVLLWMLPELNTQEFFLGRSPKEASDNGSGSEATRHS 858

RESULT 8

US-10-035-045-21

; Sequence 21, Application US/10035045

; GENERAL INFORMATION:

; APPLICANT: ADLER, JON ELLIOT

; APPLICANT: LI, XIAODONG

; APPLICANT: STASZEWSKI, LENA

; APPLICANT: O'CONNELL, SHAWN

; APPLICANT: ZOZULYA, SERGEY

; TITLE OF INVENTION: TIR TASTE RECEPTORS AND GENES ENCODING SAME

; FILE REFERENCE: 078003-0280681

; CURRENT APPLICATION NUMBER: US/10/035,045

; CURRENT FILING DATE: 2002-01-03

; PRIOR APPLICATION NUMBER: 60/259,227

; PRIOR FILING DATE: 2001-01-03

; PRIOR FILING DATE: 2001-04-19

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 21

; LENGTH: 839

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-035-045-21

Query Match

Best Local Similarity 4.7%; Score 205; DB 6; Length 839;

Matches 174; Conservative 144; Mismatches 335; Indels 244; Gaps 43;

Qy 16 FLTLCLIAHPLOGVAGRPDELHIGGFITAGKGGWQ-----GQ 55
Db 13 FLLWVIAEP--AENSDFYLPDGYLLGLFSL--HANMKGIHVHLPQVPMCKEYEVKVIY 69
Qy 56 ACPATRLADDVKNOPNLPGFKLILHSD-----SECEPGLCASVMY-----NLL-- 102
Db 70 NLQAMRFVAVEEINNDSLLPGVLLGYEIVDVYCISSNVQP-----VLYFLAHEDNLLPI 124
Qy 103 ----YKPKQLMLLAG--CSTVCTTVAEAAKMNLIIVLCYCASSPALSDKRPFPLFRTH 156
Db 125 QEDYSNYSRVAVIGPDNSESVMVANFSLFLLPQITYSAISDELDRKVRPPALLRTT 184
Qy 157 PSATVINPTRIKLMKFGNSRVAILQOAE-----EVSFTVE 193
Db 185 PSADHHVEAMVQLMHLFRWNIIIVSSDITYGRDNGOLLGERVARRDICIATFETLPTLQ 244

Query Match

4.4%; Score 190.5; DB 6; Length 852;

Qy 194 DLENRCHEAGVEIIVTROSFLSDPTDAVRNLRQDARIIVGLFVVAARRVCEMYKQOYL 253
Db 245 PNQMTSEERQRLVT-----IVDKLOQSTARVVVVVSPDLTLYHFFNEVLRQNFT 294
Qy 254 GRAHWFFI--GWYED-----NWYEVLKAEGITCTVEOMRIAAEGHLLTTEALMNQN--- 304
Db 295 GA--VWIASESWADPVLHNLTELGHTFTGITITQSVIPG-----FSEFWGPOAGPP 348
Qy 305 --NOTTISGMTAEFRHLRNLQALTEEGYDINHRYPEGYQEAFLAYDAVMSVALAFNKT 362
Db 349 PLSTQSQYTCNQECNCLNATL-----SFNTILRSGERVVSVYSAYAVAHLSLL 403
Qy 363 --ERLTGKKSLRDTTYTDKEIADIEIYAAMNSTOFLGSGVVAFSSQGDRIALTOIQMI 420
Db 404 GCDKSTCTKRVVYPW-----QLLEEIW---KVNFTLLDHQIFDPQGD--VALHL--EIV 451
Qy 421 DGKYEK-----LGYDQTQ-----LDNLSWLNTQMI-----GGK----- 449
Db 452 QMWDNRSONPFQSVASYYPQRLQKNIQDISMTVTYNNTPMCMCKRCOSGOKKPVGIH 511
Qy 450 -----VP-----QDRT-----IVTVLRVTSVLP 468
Db 512 VCCFECIDCLPGLNTEDEYEQACPNNEWSQSETSCFQRQLVFLWHEAPTIAVAL 571
Qy 469 FVCMCTISSCGIFVAFALIIFNINMKHRRVI--QSSHPVQNTIMLFGVIICLISVILLGI 526
Db 572 LAALGLFSLTALIVF-----WRHFQTPIVRSAGGPMC--FLML---TLLLVAYMVVVP 620
Qy 527 DGRFVSPEEYPKI--CQARAWLLSTGFTLAYGAMFSKVRVHRFTTKAKTDPKK---VE 581
Db 621 ---YVGP---PKVSTCLCRQALFPLCFTICISIAVRSFQIVCAFKMASRPRAYSVYWR 674
Qy 582 PWKLYTMVSGLLSDLVLLSQIFDPLQRYLETPELDPVSTDDIKRPELEHCE--SQ 640
Db 675 YQGPVSMAFITVLKMWIVVIGMLATGLSPTRTD-----DDPKI--TIVSCNPNY 724
Qy 641 RNSMGLGVYGFGLILVFLGLFLAYETRSLKVKIQRVQINDRYGMSI-----YNNVVLCLITA 696
Db 725 RNSLLFNTSLDL--LLSVVGFSAFYMGKELPT--NYEAKFTLSMTFTYFTSSVSLCTMS 781
Qy 697 PVGMVIAQQDASFAFVALAVIFCCFLSMLLI-----FVPKVEIVIRHPKDKAESKN 749
Db 782 AYSGLV-----VTIVDLLVTLNLLAISLGYFGPKCYMILFYPERNTPAYFN 828

RESULT 9

US-10-035-045-4

; Sequence 4, Application US/10035045

; GENERAL INFORMATION:

; APPLICANT: ADLER, JON ELLIOT

; APPLICANT: LI, XIAODONG

; APPLICANT: STASZEWSKI, LENA

; APPLICANT: O'CONNELL, SHAWN

; APPLICANT: ZOZULYA, SERGEY

; TITLE OF INVENTION: TIR TASTE RECEPTORS AND GENES ENCODING SAME

; FILE REFERENCE: 078003-0280681

; CURRENT APPLICATION NUMBER: US/10/035,045

; CURRENT FILING DATE: 2002-01-03

; PRIOR APPLICATION NUMBER: 60/259,227

; PRIOR FILING DATE: 2001-01-03

; PRIOR FILING DATE: 60/284,547

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 4

; LENGTH: 852

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-035-045-4

Best Local Similarity 18.98; Pred. No. 8e-08;	
Matches 173; Conservative 144; Mismatches 309; Indels 291; Gaps 43;	
QY	11 VTFWFL-----LCLIASPHLOGGVAGRDEHLHIGGIFPI--AGKGMW-----52
Db	9 LSWALLHPGTGAPCLCSOQLRMKG-----DYVLGGLFLPGAEEAGLRSRTPSPV 61
QY	53 -----GQACMPATRLALDDVNKOPNLLPGFKUILHSNDSECP--GLGASVMY-----99
Db	62 CTRESSNGLLWALAMKWAEBEINNKSDDLPLGLRLGYDLFDTCSEPVVAMKPSLFLAKAG 121
QY	100 -----NLLYNPKQLMLLAGCSTVCTTVAEAAKWNLLVL---CYGASSPALSDRKR 148
Db	122 SRDIAACNTYQYQYPRVLAVIPGHSSELAW--TCKFFSFELMPQVSYGASMELLSARET 179
QY	149 FPTLFRPHSATVNPTRIKLMKKFGKSRVAILQOAAEV-----FSTVEDLENRCH--E 201
Db	180 FPFSEFVPSDRVOLTAQAELLQFEGHNWVAALGSDDEYGRQGLSIIFSALAAARGICIAH 239
QY	202 AGVEIVTR--QSFLSDPTDAVNRLLRORDARIIVGLFVYVAARRVLCEMYKOOLYGRAHVW 259
Db	240 EGLVPLPRADDSRLKGQVDVLHQVNSQSVQVL-LFASVHA-----AHAL 283
QY	260 FFIGWYEDNWEYNLKAGITCTVEQMRIAEGHLTTAALM-----300
Db	284 FN-----YSSISRLS-----PKVWASEAWLTSLVNGLPFGMAQGTVLGFLORGA 329
QY	301 ----WNQNNOTTISGMTAEERPHRLNOALIEEG--DINHDPYE-----GY 341
Db	330 QLHEFPQVVKTHLALATDPAFCSALGER--EQGLEEDVVGORCQCOCITLQNVASAGLNH 387
QY	342 QEAPLAYDAVMSVALAKNKTMERITTG-----KKSRLDFY-----377
Db	388 HQTESVYAAYVYVAQALHNTLQCNASGCPAODPKVPQWOLLENMYNLIFHVGLPLRFDSS 447
QY	378 --TKETIADETIYAAMNSTOFTGVSQVAFVSQGDRIALTQ-----ISQIDGK 423
Db	448 GNVDMEXDLKLWVQWQSVPRLHDYGRFNGLSRTERLKIWHITSNOKPVSRCRQCQOEGQ 507
QY	424 YEKL-----GYDQTOLDNL--SWLNTQWIGGKVPQDRT-----455
Db	508 VRRVKGPHSCYDCVCEAGSYRONPDIACTFCQGEW-----SPERSTRCFRRSRFLA 563
QY	456 ----IVTHVRLTSLPLFVCMCTISSGCIFFAVALIIFINWKNHRR---VIQSSHPVCNT 508
Db	564 WGEPAVLLLLLLLSIALGL-----VLAALGLFV-----HHRDSPVQASG---GP 605
QY	509 IMLPGVI-----ICLISVILGIDGRFVSPEYPKICOARAWLLSTGFTLAYGAMFSKVMR 564
Db	606 LACFGLVCLGLVCLSVLLFPG-----QPSPARCLAQOPLSHLPLTGCLLSTLFLQAAE 657
QY	565 VHRFTTAKTDPKKVE-----PWKLYTMVSGLLSIDLLVILLSWQIFD 607
Db	658 IF-----VSESLPWADRLSGCLGRPAMLVVLLAMLV--EVALCTW-----698
QY	608 PLORYLETFPLEDPVSTTDDIKIRPE-LEHCESORNSMWL--GLVYGFKGILILVFGFLA 664
Db	699 ----YLNAFP---PEVYTDWNLHTALVHC---RTRSWSEFGLAHA-TNATLAFELFLG 747
QY	665 YETRSIKVKQINDSRVYGMGSINYVVLCLITAPYGMVIASQODASFAFVALVIFCCFLS 724
Db	748 TFLVRSQPGCYNRRAGLTFAMLAYFITWVSFVP--LLANVQVVLRPVAVQMGALLICVLG 804
QY	725 MLLIF-VPKVEIVTRHP 740
Db	805 ILAAFHILPRCYLLMRQP 821

RESULT 10
US-10-035-045-17
; Sequence 17, Application US/10035045
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT

```

; APPLICANT: LI, XIAODONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: T1R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003-0280681
; CURRENT APPLICATION NUMBER: US/10/035,045
; CURRENT FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: 60/259,227
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 60/284,547
; PRIOR FILING DATE: 2001-04-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 841
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-035-045-17

```

Query Match 4.1%; Score 180; DB 6; Length 841;
Best Local Similarity 17.8%; Pred. No. 5.7e-07;
Matches 162; Conservative 134; Mismatches 287; Indels 326; Gaps 41;

Qy	34	PDELTGGIPIAGKGW-----QGQACMPATRLALDDVNVKPNL	74
Db	35	PGDYLAGLPL--HSGCLQVRHPEVTLCDRSCSFNEHYHLFQAMRLVEEINNSTAL	92
Qy	75	LP---GFKLILHNSDE-----CEPGL-GASVMYNLLYNKPKLMLLAGCST-VC	119
Db	93	LPNITLGYQLYDYCDSPASANYATLRVLSLPGQHHEIQGLDGLHYSPTVLAVTGPPOSTNRA	152
Qy	120	TTVAEAAKMNLLVLCYGASSPALSDBRKREPTLFRTHPSATVHNPRIKLMMKFGWSRVA	179
Db	153	ATTAAALLSPFLPMISVAASSETLSVKRQVPSFLRPIPNDKYQVETWMLVLLQKFGTWS	212
Qy	180	ILQAAEVEFISTEDLENRCMEAGVEIVTR--OSFLSDPTD-----AVRNLRRODARIIV	232
Db	213	LVGSDDDYGQLGVAOLENQTGOGICIAFKDIMPFSQAQCDERMOCMLRHLAAQAGATVVV	272
Qy	233	GLFYVVAARVLCEMYKQQLYGRAHVWFYFIGWYEDNWYEVNLKAEGITCTVCEQMRIAABG	292
Db	273	---VFSSROL-----ARVFF-----ESVLT-----NLTGRV	296
Qy	293	HLTTEALMNQNTT-ISCMTAEFRHLRNLQAL-----TEEGVDINHRY	337
Db	297	WVASEA--WALSRHITGVPGI-----QRIGWGLVGAIOKRAVPGUKAFEEYARADKKA	348
Qy	338	PE-----GYOEAPLAYDAVMSVALAFNKTMERLT	366
Db	349	PRCHKSGWCSSNQLCECOAFMAHTMPKPKAFSSMSAYNAYRAVYAVAHGLHQLLGCA	408
Qy	367	TGKKSURDFTYDKEIADEIYAAMNSTQFLGSGVVAFSSQGDRIALTQIOEMIDGKYEK	426
Db	409	GACSRGRVYPW-----QLLEQIHVKVHFLHKDVTAFNDNRDPLSSYNI---IAWDWNG	458
Qy	427	LGYDTOLDNLW---LNTE-----QWIGGKVPQDRTIVTHLVRTVSLPLFCVMCTI	478
Db	459	PKWTFVLGSSSTSPQNLNETKIOMHG-----KDNQVPKSVCS---SDC	501
Qy	479	GIFVAFALIIFNINWKNHRRVQSSHPVC-----	506
Db	502	-----LEGHRVVVTFGHCCCEPCVPCGAGTFLNKSDLYRCOPCKEWPABG	548
Qy	507	-----NTIMLFG-----VIIC---LISVILLGIDGRFVSPEEYPKI	539
Db	549	SQTCFRTVVFLALREHTSWVLLAANTLILLLLGLTAGLFAWHLDTPVVSAGGRLCFLM	608
Qy	540	-----CQARWLLTSGFTLIAYGAMFSKVMR-----VHRFTTKAKT	574
Db	609	LGSIAAGSGSLYGFGEPTRPACLLRQALFALGETIFLSCLTVRSFOLLIEKFESTKYPT	668

```
QY 575 DPKKVPEPW-----KLYTMVSGLLSIDLVILLSW-QIFDPL-----QRYLETFPLEDPV 622
Db 669 -----FYHAWVNGCAGLFVNMIS--AAQLLICITLWLVVWTPLPAREYQRPPLVLMLE--- 719
QY 623 STTDDIKIRPELEHCEQSORMWGLVYGFKGLILVFLGFLAYETRSIKVKQINDSRVVG 682
Db 720 -----C-TETSLGFIPLAFLYNGLLSISAFACSYLGKDLPE-ENYNEAKCVT 763
QY 683 MS-IYNV--VLCITA-----PVGMIASOODASFAFVALAVIFCCFLSMLLIFVP 731
Db 764 FSLLENFVSWIAFTTASVYDGKYLPAANMAGLSLSSGFGG-----YFLP 810
QY 732 KVIEVIRHP 740
Db 811 KCVILCRP 819
```

```
RESULT 11
PCT-US02-07826-121
; Sequence 121, Application PC/TUS0207826
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE REFERENCE: MRI-030PC Assessment, Prevention, and Therapy of Ovarian Cancer
; CURRENT APPLICATION NUMBER: PCT/US02/07826
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-07826-121
```

```
Query Match 2.5% Score 108; DB 1; Length 403;
Best Local Similarity 19.5% Pred. No. 0.16;
Matches 50; Conservative 39; Mismatches 97; Indels 70; Gaps 9;

QY 466 LPLFVCMC-----TISCGIFVAFALIIF-----NIWNKRRVITQSSH--PVC 506
Db 42 LPQVSLCDDLAIWGIIVVEAVAGALITLLMLLILVRLPFKEKEKSPVGLHFLFL 101
QY 507 NTIMLFGVITCLISVILLGIDGRFVSPEEYPKICQARAWLLSTGFTLAYGAMFSKVRVH 566
Db 102 GTLGLFLGTLTAFTI-----QDEETICSVRRFLWGLVLCFCSCLLSQAWRVR 148
QY 567 RFTTKAKTDPKKVEPKWPKLYTMVSGLLSIDLVILLSWQIFDPLQRYLETPTPLEDPVSTTD 626
Db 149 RL-VRHGTGP-----AGWQLVGLALCLMLVQVITAVENLVLTCLR--DTRPA----- 192
QY 627 DIKIRPELEHCEQSORMWGLVYGFKGLILVFLGFLAYETRSIKVKQINDSRVVGSIY 686
Db 193 -----CAYEPMDFVMALIYDMVLLVVTGLALFTLCGKFRKWLNGA----- 234
QY 687 NVVVLCLITAPGVMI 702
Db 235 -----FULLITAFLSVLI 246
```

```
RESULT 12
US-10-097-340-121
; Sequence 121, Application US/10097340
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPARU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE REFERENCE: MRI-030 Assessment, Prevention, and Therapy of Ovarian Cancer
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-121
```

```
Query Match 2.5% Score 108; DB 6; Length 403;
Best Local Similarity 19.5% Pred. No. 0.16;
Matches 50; Conservative 39; Mismatches 97; Indels 70; Gaps 9;

QY 466 LPLFVCMC-----TISCGIFVAFALIIF-----NIWNKRRVITQSSH--PVC 506
Db 42 LPQVSLCDDLAIWGIIVVEAVAGALITLLMLLILVRLPFKEKEKSPVGLHFLFL 101
QY 507 NTIMLFGVITCLISVILLGIDGRFVSPEEYPKICQARAWLLSTGFTLAYGAMFSKVRVH 566
Db 102 GTLGLFLGTLTAFTI-----QDEETICSVRRFLWGLVLCFCSCLLSQAWRVR 148
QY 567 RFTTKAKTDPKKVEPKWPKLYTMVSGLLSIDLVILLSWQIFDPLQRYLETPTPLEDPVSTTD 626
Db 149 RL-VRHGTGP-----AGWQLVGLALCLMLVQVITAVENLVLTCLR--DTRPA----- 192
QY 627 DIKIRPELEHCEQSORMWGLVYGFKGLILVFLGFLAYETRSIKVKQINDSRVVGSIY 686
Db 193 -----CAYEPMDFVMALIYDMVLLVVTGLALFTLCGKFRKWLNGA----- 234
QY 687 NVVVLCLITAPGVMI 702
Db 235 -----FULLITAFLSVLI 246
```

Query Match 2.4%; Score 104.5; DB 1; Length 911;
Best Local Similarity 20.2%; Pred. NO. 1.1;
Matches 66; Conservative 54; Mismatches 94; Indels 113; Gaps 15;

RESULT 15
US-09-540-209B-10405
; Sequence 10405, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1001-001
; CURRENT APPLICATION NUMBER: US/09/540.209B
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 10405
; LENGTH: 498
; TYPE: prt
; ORGANISM: B.fragilis
US-09-540-209B-10405

```
Query Match      2.4%; Score 103; DB 5; Length 498;
Best Local Similarity 22.1%; Pred. No. 0.58;
Matches 67; Conservative 44; Mismatches 118; Indels 74; Gaps 14;
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Qy	215	DPTDAVNLRRQDARIIVGLFYVVAAARVLCEMKYKQLYGRA-----HWFFPIGW	264
Db	198	NPID-MDSLREQOKTVDLYNAGRKEILS---NPORYGKVTRPVRDRRENVKRCVGL	253
Qy	265	YEDNWYEYNLKAEGITCTVEQMRTIAAECHLTTEALMWNQNQTTSGMTAEEFRH----	320
Db	254	PGDTLQIIN-----GOVMIDGRAIENPENLQNFYVQTTPGYITEEMFRELGISK	303
Qy	321	LNQALIEEYDINHDPYEGVOERAPL-----AYDAWVSVALAFNTMERLTIGKKSLR	373
Db	304	ADQRLLTPEGAS-----YEEGLIELGLGRNAQGGLNPVYLPLT-KKMYDTLSGNKLVG	357
Qy	374	DFTYTDEIRIDEIYAA-MNSTQFLGVSGVAVFSOGRIALT-----Q	415
Db	358	KVIPEBEYSGEVYPNLNTHNNKSRYGPWIIPAKGATILTLDNLIPIERCITYAEGNK	417
Qy	416	IEQQMDIKY---EKLGYYDDTDLDLSWL-----NTEOWIGKGVPQODRTIVTHVLRT	463
Db	418	LEQKEDGIYINGVKTNQYTFQMD-YYYMMGDNRHNSADSRYW--GFYPEDHVWGCKPIVVW	474
Qy	464	VSL	466
Db	475	LSL	477

Query Match	2.4%	Score 104.5;	DB 1;	Length 911;
Best Local Similarity	20.2%	Pred. No. 1.1;		

Search completed: April 30, 2002, 10:15:50
Job time: 222 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:10:58 ; Search time 27.28 Seconds
(without alignments)
2280.849 Million cell updates/sec

Title: US-09-715-962-2
Perfect score: 4374
Sequence: 1 MRKDMTSDGATFWIFLCL.....LINSSAHATPRAATLAIQTGE 840

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4374	100.0	840	22	AAB86159 D. melanogaster GA
2	2035	46.5	844	19	AAW40119 Human GABA-BR1b re
3	2035	46.5	844	20	AAW28839 Human GABA-BR1b re
4	2035	46.5	844	20	AAW14102 Human GABA-BR1b re
5	2035	46.5	844	21	AAW32467 Human G-protein co
6	2034.5	46.5	899	20	AAW14107 Human GABA-BR1b re
7	2032	46.5	844	19	AAW40118 Rat GABA-BR1b re
8	2031.5	46.4	964	20	AAW14105 Canine GABA-BR1b re
9	2030.5	46.4	960	21	AAW83145 Human GABA-BR1b re
10	2030.5	46.4	961	20	AAW28838 Human GABA-BR1a re
11	2030.5	46.4	961	20	AAW29798 Human gamma-amino-

12	2030.5	46.4	961	20	AAW14101 Human GABA-BR1a re
13	2030.5	46.4	1323	20	AAW49133 Human GABA-BR1a/B
14	2029.5	46.4	793	19	AAW40117 Human GABA-BR1a re
15	2029.5	46.4	892	20	AAW14109 Human GABA-BR1a re
16	2029.5	46.4	960	19	AAW40116 Human GABA-BR1a re
17	2029	46.4	962	22	AAW50090 Murine GABA-B-R1a
18	2028.5	46.4	960	22	AAW29797 Murine gamma-amino
19	2026	46.3	844	20	AAW28842 Rat GABA-BR1b re
20	2026	46.3	844	20	AAW49123 Rat GABA-BR1b prote
21	2023.5	46.3	960	20	AAW28841 Rat GABA-BR1a re
22	2023.5	46.3	960	20	AAW49122 Rat GABA-BR1a prote
23	2023.5	46.3	960	22	AAW50089 Murine GABA-B-R1a
24	1967	45.0	886	20	AAW14110 Human GABA-BR1a re
25	1721	39.3	753	22	AAW50093 GBL protein. Caen
26	1290	29.5	941	20	AAW29796 Human gamma-amino-
27	1290	29.5	941	21	AAW90938 Human GABA-B re
28	1290	29.5	941	21	AAW51928 Human GABA-B re
29	1290	29.5	941	21	AAW70328 Human GABA-B-R2 re
30	1290	29.5	941	21	AAW79202 Human GABA-B re
31	1290	29.5	941	21	AAW44342 Human GABA-B re
32	1290	29.5	941	22	AAW50088 HG20 protein sequ
33	1290	29.5	943	20	AAW28837 Human GABA-BR2 re
34	1289	29.5	941	21	AAW68743 A human gamma-amin
35	1287	29.4	940	21	AAW44343 Rat GABA-B re
36	1285.5	29.4	914	21	AAW44344 Protein-1 related
37	1285.5	29.4	965	21	AAW44345 Protein-2 related
38	1285	29.4	1303	20	AAW49132 Human GABA-BR2 fusi
39	1284	29.4	898	20	AAW14082 Human GABA-BR2 prot
40	1284	29.4	898	21	AAW70326 Human gamma-amino
41	1283	29.3	940	21	AAW90937 Rat GABA-B re
42	1283	29.3	940	21	AAW70327 Rat gamma-amino bu
43	1282	29.3	940	21	AAW51927 Rat GABA-B re
44	1263	28.9	883	20	AAW14081 Rat GABA-BR2 protei
45	1249.5	28.6	473	20	AAW49107 Human GABA-BR1b ext

ALIGNMENTS

RESULT 1	
AAB86159	
ID AAB86159	standard; Protein; 840 AA.
XX	
AC AAB86159;	
XX	
DT 03-AUG-2001	(first entry)
XX	
DE D. melanogaster	GABA-B receptor protein SEQ ID 2.
XX	
KW GABA-B receptor; fruitfly; gamma-aminobutyric acid B receptor;	
KW insecticide; transgenic invertebrate; plant protection agent;	
KW human medicine; veterinary medicine; insect.	
XX	
OS Drosophila melanogaster.	
XX	
PN DE19955408-A1.	
XX	
PD 23-MAY-2001.	
XX	
PF 18-NOV-1999;	99DE-1055408.
XX	
PR 18-NOV-1999;	99DE-1055408.
XX	
PA (FARB) BAYER AG.	
XX	
PI Raming K, Mezler M, Mueller T;	
XX	
DR WPI: 2001-318282/34.	
DR N-PSDB; AAH20519.	
XX	
PT New invertebrate gamma-aminobutyric acid receptor proteins, useful in	
PT screening for potential insecticides, for plant protection or medicine,	
PT also related nucleic acid	

XX Claim 2: Page 16-21; 62pp; German.
PS This invention describes a novel polypeptide (I), functioning as a
CC gamma-aminobutyric acid -B (GABA-B) receptor which has insecticidal
CC activity. (I), also the nucleic acid (II) that encodes it and related
CC vectors, host cells, antibodies and transgenic invertebrates, are used
CC for identifying: (i) new plant protection agents, i.e. modulators of (I)
CC with insecticidal activity, which may also be useful in human or
CC veterinary medicine; and (ii) genes that encode polypeptides involved in
CC assembly of functionally related GABA-B receptors in insects. This
CC sequence represents a fruitfly (*Drosophila melanogaster*) GABA-B receptor
CC which is described in the method of the invention.
XX
SQ Sequence 840 AA;

Query Match 100.0%; Score 4374; DB 22; Length 840;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKRDMTSDGAVTFWIFLLCLLIAGPHLGGVAGRPDELHIGIPIAGKGGWGGACMPA 60
Db 1 mkrdmtsdgavtfwifllclliagphlgggvagrpdelhigifpiagkgggwggacmpa 60

Qy 61 TRIALDDVKNQPNLPGFKLILHSNDSECEPGLGASVYMYNLLYNKPKMLLAGCSTVCT 120
Db 61 trlaldvknqpnlpfgkllilhsndsecepglgasvymynllynkpkmlllagcstvtc 120

Qy 121 TVAEAAKMNLIIVLCYGASSPALSDRKRFPTLFRTHPSAVHNPTRIKLMKKFGWSRAI 180
Db 121 tvaeaaakmnliivlcygasspalssdrkrfptlfrthpsatvhnptriklmkkfgwsrai 180

Qy 181 LQAEVFTSTVEDLENRCMEAGVEIVTROSFLSDPTDAVRNLRRODARIIVGLFYVAA 240
Db 181 lqaeveftstvedlenrcmeagveivtrgsflsdptdavrnlrrordariivglfyvaa 240

Qy 241 RRVLCMEYKQQLYGRAHVPFFIGWYEDNWEVNLKAEGITCTVEQMRIAEGHLLTTEALM 300
Db 241 rrvlcemykqqlgrahvpffigwyednwevnlkaegitctveqmrriaeghllttealm 300

Qy 301 WNQNNOTTISGMTAEFRHRLNQLAIEEGYDINHRYPEGYQAEPLAYDAVWSVALAFNK 360
Db 301 wqnqnttisgmtaeefrhrlnqllaeegydinhdrypegyqaeplaydavwsvalafnk 360

Qy 361 TNERLTGKSLPDPFYTDKEIADEIYAANNSTQFLGSGVWAFSSGGDRIALTQIQEMI 420
Db 361 tnerltgkkslpdpfytdkeiadeiyaannstqflgsgvwafssggdrialtqieqmi 420

Qy 421 DGKYEKLYGYDTOLDNLISWLTQEWIGGKVPQDRITVTHVLTSLPLFCVMCTISSCGI 480
Db 421 dgkyeklygydytoldnliswltqewigggkvpqdritythvltslplfvcmtisscgi 480

Qy 481 FVAFALIIFNIWNKRRVIOSSHPVCNTIMLFGVILICISVILGIDGRFVSPEEYKIC 540
Db 481 fvafaliiifniwnkrrviqsshpvcntimlfgvilicisvillgidgrfvspeeypkic 540

Qy 541 QARAWLLSTGFTLAYGAMFSKVRVHRFTTKAKTDPKKVEPWKLYTWVSGLLSIDLVIL 600
Db 541 qarawllstgftlaygamfskvrhrfttkaktdppkkvepwklytwvsgllsidvil 600

Qy 601 LSWQIFDPLQRYLETFTPLEDPVSTDDIKIRPELEHCEESNMSWMLGLVYGFGLILVFG 660
Db 601 lswqifdplqryletftpledpvstddikirpelehesesnmswmlglvygfglilvfg 660

Qy 661 LFLAYETRSIKVKQINDSRVVGMSIYNVVLCLITAPVGMVIAISQOQASFAVALAVFC 720
Db 661 lflayetrsikvkqindsrvgmsiynvvlclitapvgmviasqoqasfafvalavfc 720

Qy 721 CFLSMILLIFVPKVIEWIRHPKDAESKYNPDSDAISKEDEERYOKLVTENEOLQLRIQKE 780
Db 721 cflsmillifvpkviewirhpkdaeskynpdpsaiskedeeryoklvteneolqlriqke 780

Qy 781 EKIRVLRORLYVERGDAGKTELGATGVSAAVAATTSSQASLINSSAHATPAATLAIQTGE 840
Db 781 ekirvlrqlrvlvergdahtelngatgvsaaavattssqaslinssahatpaatlaigtge 840

RESULT 2
AAW40119
ID AAW40119 standard; Protein; 844 AA.
XX AC AAW40119;
XX 03-JUN-1998 (first entry)
XX Human GABA-BR1b receptor protein.
XX Gamma-aminobutyric acid; GABA-BR1a/b receptor; human; brain; agonist;
KW inhibitory neurotransmitter; peripheral nervous system; antagonist;
KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
KW epilepsy; cognitive function.
XX Homo sapiens.
XX WO9746675-A1.
XX 11-DEC-1997.
XX 19-MAR-1997; 97WO-EP01370.
XX 22-NOV-1996; 96US-0756091.
XX 30-MAY-1996; 96US-0655716.
XX (NOVS) NOVARTIS AG.
XX Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;
XX WPI; 1998-042183/04.
XX N-PSDB; AAV10267.
XX Purified GABA-B receptor or receptor protein - and antagonists of
XX these which may be useful in treating nervous system disorders
XX Claim 4; Page 86-90; 108pp; English.
XX This sequence represents a novel human GABA-B receptor protein,
XX GABA-BR1b. GABA (gamma-aminobutyric acid) is the major inhibitory
XX neurotransmitter found in the brain and peripheral nervous system
XX and this receptor may be used for the identification of GABA-B
XX receptor agonists and antagonists. Such proteins may be used in
XX treatment of dementia, depression, anxiety, epilepsy, spasticity,
XX bronchial inflammation or asthma or to improve cognitive function.
XX GABA-B receptor ligands and probes derived from this sequence can be
XX used to assay for GABA-B receptors or DNA encoding them.
XX Sequence 844 AA;

Query Match 46.5%; Score 2035; DB 19; Length 844;
Best Local Similarity 49.3%; Pred. No. 7.5e-193;
Matches 387; Conservative 151; Mismatches 219; Indels 28; Gaps 9;

Qy 23 SPHL---QGVAGRDE----LHIGIFPIAGKGGWGGACMPATRLALDDVKNQPNLL 75
Db 32 sphlprhsrvpphserravvialgfms--ggwpgggacqpavemaedvnsrrdil 89

Qy 76 PGFKLILHSNDSECEPGLGASVYMYNLLYNKPKMLLAGCSTVCTTVAAKAMNLIIVLC 135
Db 90 pdeylklilhsndskdpqgatkyllylndypikilmpgcssvstivaearmnlvils 149

Qy 136 YGASSPALSDRKRFPTLFRTHPSAVHNPTRIKLMKKFGWSRAIILQOAEVFTSTVEDL 195
Db 150 ygasspalssdrkrfptlfrthpsatvhnptriklmkkfgwsraifstltdl 209

Qy 196 ENRCMEAGVEIVTROSFLSDPTDAVRNLRRODARIIVGLFYVVAARRVLCMEYKQLYGR 255

Db 210 eervkeagieitfrqsfpspavpvnkqdarilvglyfetearkvfcvkerlfgk 269
 QY 256 AHVWFFIGWYEDNWEVNLKAEIGTCTVEQMRIAAEGLHTEALMWNONNQTTSGMTAE 315
 Db 270 kywvfligwyadnwfk1--ydpnsinctvdeanteaveghitteivmlpantrsisnmtsq 327
 QY 316 EFRHRLNQAIEEGYDINHRYPE---GYQEAPLAYDAVMSVALAFNKTMERLTGKSL 372
 Db 328 efvekltkrl-----krhpeetgfgqepalaydaialalalnktsgggrsgvrl 378
 QY 373 RDTYTDKEIADEIYAAMNSTQFLGVGVAFSSQGDRIALTOIEQMDGKYEKLYGVD 432
 Db 379 edfnyntqitldqiyramsssfegsvghvfdasgrmawtlieqlggysykgigyds 438
 QY 433 QLDNLWLNTEQWIGKVPQDRTIVTHVLTSLPLFVCMCTISSCGIFVAFALIIFNW 492
 Db 439 tkddlsksktdkwiggspadqlviktfflsqklfisvsvlsslgivlavvcslfniy 498
 QY 493 NKHRRVIOSSHPCVNTIMLFGVILCLISVILLGIDGRFVSPPEYPKICQARALLSTGFT 552
 Db 499 nshvryiqnsqpnlnltavgcslalaavfplgdgyhigrngfpvcqarlwlilgifs 558
 QY 553 LAYGAMESKVRWVRHRTTK--AKTDPKKVPEPKLYTMVSGLLSIDLVILLSMQIEDPLQ 610
 Db 559 lgygsmftkiwwhtvftkkekewrktlepkiyatvgllvgmdvitaiwqivdplh 618
 QY 611 RYLETFPLEDPVSTDDIKIRPELEHCEQSQRNSMWGLVYGFKGLIILVFLFLAYETRSI 670
 Db 619 rtietfakeepkedi-dvslilpqlehcscrkmtwtgifygkglllilgflayetsk 677
 QY 671 KVKQINDSRYVGMISYNNVVLITAPVGMVIA SQDASAFVALAVIFCCFLSMLIFV 730
 Db 678 stekindhavgmalyvnavvlclitapvtmilssqgdaafafaslaivfsyitlvlfv 737
 QY 731 PKVIEVIRHP--KDKAESKYNPDSAISKEDERYQKLVITENEQLRLITQEEKIRVL 788
 Db 738 pxmrilrtgwgseagdtmktgssntnnneeksrllenenrelekiiaekeervselrh 797
 QY 789 RLVER 793
 Db 798 qlqsr 802
 RESULT 3
 ID AAY28839
 XX AAY28839 standard; Protein; 844 AA.
 XX AC AAY28839;
 XX DF 17-JAN-2000 (first entry)
 XX DE Human GABABR1b receptor protein.
 XX KW GABABR1b receptor protein; cloning; rat brain; GABABR2; GABAB receptor;
 KW human gamma-aminobutyric acid receptor; metabotropic receptor; screening;
 KW synaptic transmission; GABABR1b; cloned receptor; splice variant;
 KW modulatory agent; molecular activity assay; antispastic; anti-addictive;
 KW antineurodegeneration; analgesic; cardiovascular activity.
 XX OS Homo sapiens.
 XX PN W09591636-A2.
 XX PD 14-OCT-1999.
 XX PF 02-APR-1999; 99WO-US07352.
 XX PR 03-APR-1998; 98US-0080676.
 XX PA (NPSP-) NPS PHARM INC.
 XX PI Garrett JE, Simin RT, Busby JG, Stormann TM;

XX WPI; 1999-610994/52.
 DR N-PSDB; AAX90921.
 XX Novel nucleic acids, used to screen for specific modulators, e.g. for
 PT treating spasticity or Alzheimer's disease -
 XX Disclosure; Fig 2A-2E; 78pp; English.
 XX The present sequence encodes GABABR1b receptor protein cloned from rat
 CC brain. This is closely related to GABABR2. GABAB receptors are
 CC metabotropic receptors that modulate synaptic transmission in brain.
 CC GABABR1a differs from GABABR1b in that the N-terminal 147 residues are
 CC replaced by 18 amino acids. Both of these cloned receptors appear to be
 CC splice variants. They are expressed in cells that express GABABR2. This
 CC nucleotide sequence is used to screen for specific modulators. These
 CC modulators have antispastic, antineurodegeneration, analgesic, anti
 CC -addictive, cardiovascular activities.
 CC Note: SEQ ID NO. 8 is referred as the GABABR1a receptor protein in
 CC the specification.
 XX Sequence 844 AA;
 SQ
 Query Match 46.5%; Score 2035; DB 20; Length 844;
 Best Local Similarity 49.3%; Pred. No. 7.5e-193;
 Matches 387; Conservative 151; Mismatches 219; Indels 28; Gaps 9;
 QY 23 SPHL---GGVAGRPDE---LHIGGIPPIACKGQGGOGACMPATRLALDDVKNQPNLL 75
 Db 32 sphlprhsrvpphserravyigalfpms--ggwpggqacqavemaalevdnsrrdl 89
 QY 76 PGFKLILHSNDECPGPGASVWYNLLNKPQKMLLAGCSTVCTVTAFAAKMNLIVLC 135
 Db 90 pdyelkllhhdskdpqgatkyllylndpikilmpgcssvstlvaaearmwnlivls 149
 QY 136 YGASSPALSDKRFPPTLFTPHSPATVHNPTRIKLMKKGWSRVAILQAEYFISTVEDL 195
 Db 150 ygssspalsnqrftfrthpsatlhnptrvklfekwgwkkiatigqtevtftldld 209
 QY 196 ENRCMEAGVIVTRQSFSLSDPTDAVRLNRQDARITVGLFVYVVAARRVLCMEYKQOLYGR 255
 Db 210 eervkeagieitfrqsfpspavpvnkqdarilvglyfetearkvfcvkerlfgk 269
 QY 256 AHVWFFIGWYEDNWEVNLKAEIGTCTVEQMRIAAEGLHTEALMWNONNQTTSGMTAE 315
 Db 270 kywvfligwyadnwfk1--ydpnsinctvdeanteaveghitteivmlpantrsisnmtsq 327
 QY 316 EFRHRLNQAIEEGYDINHRYPE---GYQEAPLAYDAVMSVALAFNKTMERLTGKSL 372
 Db 328 efvekltkrl-----krhpeetgfgqepalaydaialalalnktsgggrsgvrl 378
 QY 373 RDTYTDKEIADEIYAAMNSTQFLGVGVAFSSQGDRIALTOIEQMDGKYEKLYGVD 432
 Db 379 edfnyntqitldqiyramsssfegsvghvfdasgrmawtlieqlggysykgigyds 438
 QY 433 QLDNLWLNTEQWIGKVPQDRTIVTHVLTSLPLFVCMCTISSCGIFVAFALIIFNW 492
 Db 439 tkddlsksktdkwiggspadqlviktfflsqklfisvsvlsslgivlavvcslfniy 498
 QY 493 NKHRRVIOSSHPCVNTIMLFGVILCLISVILLGIDGRFVSPPEYPKICQARALLSTGFT 552
 Db 499 nshvryiqnsqpnlnltavgcslalaavfplgdgyhigrngfpvcqarlwlilgifs 558
 QY 553 LAYGAMESKVRWVRHRTTK--AKTDPKKVPEPKLYTMVSGLLSIDLVILLSMQIEDPLQ 610
 Db 559 lgygsmftkiwwhtvftkkekewrktlepkiyatvgllvgmdvitaiwqivdplh 618
 QY 611 RYLETFPLEDPVSTDDIKIRPELEHCEQSQRNSMWGLVYGFKGLIILVFLFLAYETRSI 670
 Db 619 rtietfakeepkedi-dvslilpqlehcscrkmtwtgifygkglllilgflayetsk 677
 QY 671 KVKQINDSRYVGMISYNNVVLITAPVGMVIA SQDASAFVALAVIFCCFLSMLIFV 730

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Db 678 stekindhavmagiynvavclitapvtmllsqdaafafalaivfssyilvlfv 737
Qy 731 PKVIEVIRHP--KDKAESKYNPDSAISKEDEERYOKLVTENEQLRLITQKEEKIRVLQ 788
Db 738 pkmrllitrgewqseaqdtmktgssntnnneeksrlllekenrelekiiaekeervselrh 797
Qy 789 RLVER 793
Db 798 qlqsr 802

RESULT 4
ID AAY14102 standard; Protein; 844 AA.
AC AAY14102;
XX
DT 21-JUL-1999 (first entry)
XX
DE Human GABAB receptor lb protein sequence.
XX
KW GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;
KW transient lower oesophageal sphincter relaxation; spasticity; emesis;
KW gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;
KW irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;
KW autoimmune disease; neoplastic disease; infectious disease; therapy.
XX
OS Homo sapiens.
XX
PN WO9921890-A1.
PD
PE 06-MAY-1999.
PF 27-OCT-1998; 98WO-SF01947.
PR 17-JUL-1998; 98SE-0002575.
PR 27-OCT-1997; 97SE-0003914.
PR 16-MAR-1998; 98SE-0000864.
XX
PA (ASTR ) ASTRA AB.
XX
PI Ekstrand J;
XX
DR WPI; 1999-302985/25.
DR N-PSDB; AAX58055.
XX
PT Polynucleotides encoding human and canine gamma aminobutyric acid
PT type B receptors, used to screen for compounds that are inhibitors
PT of transient lower oesophageal sphincter relaxations
PS Claim 17; Page 90-94; 222pp; English.
XX
CC This sequence is a human gamma aminobutyric acid type B (GABAB)
CC receptor of the invention. Nucleic acid molecules encoding GABAB
CC receptors can be used to screen for compounds that are inhibitors of
CC transient lower oesophageal sphincter relaxations (TLESR). They can also
CC be used to screen for agonists or antagonists of the GABAB receptors.
CC Inhibitors of TLESR are useful for treating gastro-oesophageal reflux
CC disease. Other uses of GABAB receptors, such as human GABAB R1c or 1d,
CC comprise diagnosis or treatment of conditions related to GABAB
CC dysfunction, e.g. epilepsy, psychiatric disorders, emesis, irritable
CC bowel syndrome, dyspepsia, spasticity, arthritis, allergies, autoimmune
CC diseases, neoplastic diseases, pain and infectious disease.
XX
SQ Sequence 844 AA;

Query Match 46.5%; Score 2035; DB 20; Length 844;
Best Local Similarity 49.3%; Pred. No. 7.5e-193;
Matches 387; Conservative 151; Mismatches 219; Indels 28; Gaps 9;
Qy 23 SPHL---QGVAGRDE---LHTGIFPIAGKGGWGGQACMPATRLALDDVKNQPNLL 75
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Db 32 sphlprphspphserravyigalfpms--ggwpgggacqavameadenvsrddil 89
Qy 76 PGFKLILHSNDECPGLGASVWYLLNKPQKMLLAGCSTVCTTVAEAAKMWNLIVLC 135
Db 90 pdyelkllhdsdkdpqgatkyllyllyndpikilimpacssvstlvaearmwnlivls 149
Qy 136 YGASSPALSDRRKRPPTLFRTHPSATVHNPTRIKLMKFGWSVAILQQAEEVFISTVDL 195
Db 150 ygssspalsnqrfrptfrthpsatlhnptrvklfekgwkkklatiqgtteftstldl 209
Qy 196 ENRCMEAGVEIVTROSLSDPTDAVNLRRQDARIIVGLFVYVVAARRVLCENYKQOYLGR 255
Db 210 eervkeagietfrqsfdsdpavpvknkrqdarliivgifyetearkvicevykerlfqk 269
Qy 256 AHVFEFIGWYEDNWYEVLNKAEGITCTVBOMRIAAEGHLLTTEALMWNQNNQTTISQMTAE 315
Db 270 kyvfwligwadnwfkii--ydpisinctvdemteaveghitteivmlnpantrisismtsq 327
Qy 316 EFRHRLNQAALIEEYDINHRYPE---GYOEAPLAYDAYVMSVALAFNPKTMERLTTGKKSL 372
Db 328 efvekltkrl-----krhpeetggfgeaplaydaiwalalalnktsggggrsgvrl 378
Qy 373 RDTFTYDKEIADEIYAAMNSTOFLGVSGVAVFSSQGDRIALTQIEQIDGKYEKLGYYDT 432
Db 379 edfnyndqtdqlyramnsssfegvshvfdasgsrmawtliedlqggysykkigydds 438
Qy 433 QLDNLISWLNTEQWIGGKVPQDRITVTHVLRTVSLPLFVCMCTISSCGIFVAFALIFNINW 492
Db 439 tkddlsawktdkwiggspadqlviktkfrfiskqlfsvsvisslgvlavvcisfnly 498
Qy 493 NKHRRVIQSSHPVCNTIMLFGVIIICLISVILGIDGRFVSPEEYPRKICQARAWLLSTGPT 552
Db 499 nshvryiqnsqnlmltavgcslalaaavplgldyghgrnqpfvcqariwlglgfs 558
Qy 553 LAYGAMFSKVMVRVHREPTTK--AKTDPKKKVEPWKLYTMVSGLLSIDLVILLSQWIPDPIQ 610
Db 559 lgygsmfktkwvhtvftkkekewrktlepkklyatvgllvgmdvltlaiwqivdplh 618
Qy 611 RYLETFPLEDPVSTTDDIKIRPELEHCEQSQRNSMNLGLVYGFKGLLVFLFLPAYETRSI 670
Db 619 rtietfakeepkedl--dvsilpqlecnscsrkmtwtlgyfygkglilllgliflayetksv 677
Qy 671 KVKQINDSRVGMISYNNVVVLCLITAPVGMVIAQQDASFAFVALAVIFCCFLSMLLIFV 730
Db 678 stekindhavmagiynvavclitapvtmllsqdaafafalaivfssyilvlfv 737
Qy 731 PKVIEVIRHP--KDKAESKYNPDSAISKEDEERYOKLVTENEQLRLITQKEEKIRVLQ 788
Db 738 pkmrllitrgewqseaqdtmktgssntnnneeksrlllekenrelekiiaekeervselrh 797
Qy 789 RLVER 793
Db 798 qlqsr 802

RESULT 5
ID AAY32467 standard; Protein; 844 AA.
XX
AC AAY32467;
XX
DT 27-MAR-2000 (first entry)
XX
DE Human G-protein coupled receptor GABAB1b.
XX
KW GABAB1b; G-protein coupled receptor; human; antibacterial;
KW antiviral; virucide; antiparasitic; analgesic; cytostatic;
KW antidiabetic; anorectic; cardiant; antiparkinsonian;
KW hypertensive; hypotensive; antiemetic; osteopathic; antianginal;
KW cerebroprotective; antiulcer; antiallergic; neuroleptic;
KW tranquilizer; antidepressant; nootropic; antimigraine;
KW anticonvulsant; neuroleptic; agonist; antagonist; inhibitor;
```



```
QY 191 TVEDLENRCMEAGVEIVTROSFLSDPTDAVRLNRRODARIIVGLFYVVAARRVLCEMYKQ 250
   I::III I IIII III IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 205 tldleervkeagietfrgssfdpavpvknkrqdarliivglfyetearkvfveyke 264
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
QY 251 QLYGRAHVWFITGWYEDNVEVNLKAEIGTCTVEOMRIAAEGHLLTTEALMWNQNNOTTIS 310
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 265 rlfqkywvfligwadnwftk--ydpinctveemteaveghitteivmlnpantris 322
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
QY 311 GMTAEFRHRLNQALIEGYDINHRYPE---GYQEAPLAYDAVMSVALAFNKTMERLTT 367
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 323 nmtsgefvekltrl-----krhpeetggfgeaplaydaiwalalalnktsgggr 373
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
QY 368 GKSLRDFYTTKEIADEIYAAMNSTQFLGSGVWAFSPSGODRIALTQIOMIDGKYEKL 427
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 374 sgvrledfnnnqitdqiyramnsssfegshvvdasgrmawtlieqlggsykki 433
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
QY 428 GXYDTOLDNLWLTQEWIGGKVPQDRTIVTHVRLVSLPFCVCMCTISSCGIFVAFALI 487
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 434 gyydstkddslwsktdkwlggspadqtlvktfrfslkfsvslsslgivlavvcl 493
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
QY 488 IFNIWNKRRVQSSHPVQNTIMLFGVIICLSVILGIDGRFVSPREYPKICQARAWLL 547
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 494 sfniynshvryiqnspnlnltavgcslalaaavfplgdgyhigrsqfvcqarlwl 553
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
QY 548 STGFTLAYGAMPKSVWRVHRTTK--AKTDPKKKVPWKLYTMVSGLLSIDLVILLSQOI 605
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 554 glfslgygsmfkiwvhtvfkkeekewrktlepwklyatvgllvgmdvltlaiwqi 613
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
QY 606 FDPLORYLTFPLEDPVSTDDIKIRPELEHCESORNSMHLGLVYGFKGLILVFGFLAY 665
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 614 vdlplrltiefakeepkedi-dvsilplqehcsskmtwlgfygykgllllgflay 672
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
QY 666 ETRSRVKOINDSRVYVGMSTYVWVLCITAPYGMVITASOODASFAVALAVIFCCFLSM 725
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 673 ektsvstekindhvragmaynvavilclitcapvtmlssqgdaafaslaivfssyiti 732
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
QY 726 LLIFFVPKIVIEVHRPKDKAESK--YNPDSAISKEDERYOKLVTEBNQLRLITQKEKI 783
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 733 vvlfpkmlrlitrgewqsetqtdmtgtsstnnneeksrllekenrelekiiaekeerv 792
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
QY 784 RVLRQLVER 793
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 793 selrhqlqsr 802
   I::III I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII

RESULT 8
ID AAY14105 standard; Protein; 964 AA.
XX AC AAY14105;
XX AC AAY14105;
XX DT 21-JUL-1999 (first entry)
XX DE Canine GABAB receptor la protein sequence.
XX DE GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;
KW transient lower oesophageal sphincter relaxation; spasticity; emesis;
KW gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;
KW irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;
KW autoimmune disease; neoplastic disease; infectious disease; therapy.
XX OS Canis familiaris.
XX XX WO9921890-A1.
XX PD 06-MAY-1999.
XX XX 27-OCT-1998; 98WO-SE01947.
XX XX 17-JUL-1998; 98SE-0002575.
XX PR 27-OCT-1997; 97SE-0003914.
XX PR 16-MAR-1998; 98SE-0000864.
```

XX (ASTR) ASTRA AB.

XX Ekstrand J;

XX WPI: 1999-302985/25.

XX N-PSDB; AAX58058.

XX Polynucleotides encoding human and canine gamma aminobutyric acid
PT type B receptors, used to screen for compounds that are inhibitors
PT of transient lower oesophageal sphincter relaxations

XX Claim 17; Page 99-105; 222pp; English.

XX This sequence is a canine gamma aminobutyric acid type B (GABAB)
CC receptor of the invention. Nucleic acid molecules encoding GABAB
CC receptors can be used to screen for compounds that are inhibitors of
CC transient lower oesophageal sphincter relaxations (TLESR). They can also
CC be used to screen for agonists or antagonists of the GABAB receptors.
CC Inhibitors of TLESR are useful for treating gastro-oesophageal reflux
CC disease. Other uses of GABAB receptors, such as human GABAB R1c or 1d,
CC comprise diagnosis or treatment of conditions related to GABAB
CC dysfunction, e.g. epilepsy, psychiatric disorders, emesis, irritable
CC bowel syndrome, dyspepsia, spasticity, arthritis, allergies, autoimmune
CC diseases, neoplastic diseases, pain and infectious disease.

XX Sequence 964 AA;

Query Match 46.4%; Score 2031.5; DB 20; Length 964;

Best Local Similarity 49.4%; Pred. No. 2.le-192;

Matches 386; Conservative 152; Mismatches 216; Indels 27; Gaps 9;

QY 24 PHLGGVAGRDE----LHIGIRPIACKGGWGGGOACMPATRLALDDVKNKPNLLPGPK 79

Db 158 phqc--vstphserravyigalfpms--ggwpgggacqapavemaledvnsrrdlpdye 213

QY 80 LILHNSDECEPGLGASVYNNLLNKPQKMLLAGCSTVCTTVAAAKMNNLIVLCYGAS 139

Db 214 lklihdskcdpgqatkyllylndypikilimpgcsvstvaeaarmnllivisygss 273

QY 140 SPALSDRRFPTLFRTHPSATVHNPTRIKMKKFWRSVAIILOQAEVEFISVDELENRC 199

Db 274 spalsnrgfrptftrhpsatlhnptrvklfekwgrkiatigqteftstldleerv 333

QY 200 MEAGVEIVTROSFLSDPTDAVRLNRRODARIIVGLFYVVAARRVLCEMYKOLYGRAHVW 259

Db 334 keagietfrgssfdpavpvknkrqdarliivglfyetearkvfveykerlfqkyvw 393

QY 260 FFIGWYEDNWEVNLKAEIGTCTVEQMRIAABGHLLTTEALMWNQNNOTTISGMTAEFRH 319

Db 394 fligwadnwftk--ydpinctvdeemteaveghitteivmlnpantrisnmtsgfve 451

QY 320 RLNQALIEEGYDINHRYPE---GYQEAPLAYDAVMSVALAFNKTMERLTTGKKSLRDT 376

Db 452 kltrl-----krhpeetggfgeaplaydaiwalalalnktsggsgsgvrledfn 502

QY 377 YTDKEIADEIYAAMNSTQFLGSGVWAFSPSGODRIALTQIOMIDGKYEKLGYDTQDN 436

Db 503 ynnqitdqiyramnsssfegshvvdasgrmawtlieqlggsykkiyydstkdd 562

QY 437 LSWLNTQEWIGKVPQDRTIVTHVRLVSLPFCVCMCTISSCGIFVAFALIIFNIWNKHR 496

Db 563 lswsktdkwiggappadqtlvktfrfmsqklfsvslsslgivlavvclsfnlvshv 622

QY 497 RVIOSSHVPVCNTIMLFGVIICLSVILGIDGRFVSPREYPKICQARAWLLSTGFTLAYG 556

Db 623 ryiqnspnlnltavgcslalaaavfplgdgyhigrsqfvcqarlwlilglgslgy 682

QY 557 AMFSKVRVHRTTK--AKTDPKKKVPWKLYTMVSGLLSIDLVILLSQWFDPLQRYLE 614

Db 683 smfktkiwvhtvfkkeekewrktlepwklyttvgllvgmdvltlaiwqmvdpvdlhrtie 742

QY 615 TPLEDPVSTTDKIRPELEHCSORNSMWLGVLGVGFKGLILVFLGFLAYETRSIKVKO 674
 DB 743 tfakeepkedi-dvsilpqlhecsskmtwlgfygkglililgflayetskvsstek 801
 QY 675 INDSRYVGSIIYVNVVLCLITAPVGMVIAQQDASFAFALAVIFCCFLSMLLIFVPKVI 734
 DB 802 indhravgmamynvavclitapvtmilsqqdaafafaalaivfssyiltvlvfpkmr 861
 QY 735 EVIRHP--KDKAESKYNPDSAISKDEERYQKLVITENEQRLITQKEKIRVLQRBLE 792
 DB 862 rlitrgewdseqdtkmtgstnneeksrlllekenrelekiiaekervselrhqlrs 921
 QY 793 R 793
 DB 922 r 922

RESULT 9
 AAY83145
 ID AAY83145 standard; Protein; 960 AA.
 AC AAY83145;
 XX
 DT 24-JUL-2000 (first entry)
 XX
 DE Human GABAB1A receptor.
 XX
 KW GABAB1A receptor; G-protein; disease; treatment; detection;
 KW therapy; antibody; immune response; infection; cancer; diabetes;
 KW obesity; anorexia; bulimia; Parkinson's disease; heart failure;
 KW hypotension; hypertension; urinary retention; osteoporosis;
 KW angina pectoris; myocardial infarction; stroke; asthma;
 KW allergy; benign prostatic hypertrophy; migraine;
 KW neurological disorders including anxiety; schizophrenia;
 KW depression; dementia; Huntington's disease;
 KW Gilles de la Tourette's syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200012106-A1.
 XX
 PD 09-MAR-2000.
 XX
 PF 30-AUG-1999; 99WO-US19435.
 XX
 PR 01-SEP-1998; 98US-0144779.
 XX
 PA (SMTK) SMITHKLINE BEECHAM CORP.
 XX
 PI Elshourbagy NA;
 XX
 DR WPI: 2000-237771/20.
 DR N-PSDB; AA293411.
 XX

PT New GABAB1A polypeptide useful for diagnosis, treatment and prevention
 of diseases associated with its expression including infections,
 psychotic and neurological disorders and cancer
 PT
 PT
 XX
 PS Claim 1; Page 34-36; 38pp; English.

CC The GABAB1A receptor is believed to be a member of the GABAB
 family of polypeptides. They are therefore of interest because
 members of the purinergic 7m receptor family (G-protein coupled
 receptors) of genes are involved in a number of biological and
 disease manifestations. They are also a successful target for
 pharmaceutical intervention. Antibodies directed against GABAB1A
 and its peptides can be used to treat bacterial, fungal, protozoan
 and viral infections, pain, cancers, diabetes, obesity, anorexia,
 bulimia, Parkinson's disease, acute heart failure, hypotension,
 hypertension, urinary retention, osteoporosis, angina pectoris,
 myocardial infarction, stroke, ulcers, asthma, allergies, benign
 prostatic hypertrophy, migraine, vomiting, psychotic and
 neurological disorders including anxiety, schizophrenia, depression,

CC dementia and severe mental retardation and dyskinesias such as
 CC Huntington's disease or Gilles de la Tourette's syndrome. The
 CC GABAB1A polypeptide or a vector comprising a sequence encoding the
 CC polypeptide can be used to induce an immunological response in a
 CC mammal to protect against disease. The presence or absence of a
 CC mutation in the nucleotide sequence encoding the GABAB1A polypeptide
 CC can be detected in the genome of a subject and/or the presence or
 CC amount of expression of the polypeptide in a sample from the subject
 CC can be analysed and used to diagnose a disease or susceptibility to a
 CC disease related to the expression or activity of GABAB1A.
 CC Diagnosis can be measured at the RNA level using nucleic acid
 CC amplification, e.g. polymerase chain reaction, RNase protection or
 CC Northern blotting or at the protein level by radioimmunoassay,
 CC competitive-binding assays, Western blot analysis or ELISA assays
 CC (enzyme linked immunosorbent assay).
 XX

SQ Sequence 960 AA;

Query Match 46.4%; Score 2030.5; DB 21; Length 960;
 Best Local Similarity 49.3%; Pred. No. 2.6e-192;
 Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;

QY 24 PHLQGGVAGRPDE--LHIGGIPPIAGKGGGQGGQACMPATRLALDDVAKQPNLLPGFKLI 81
 DB 154 phcqvnrtpsherravyigalfpms--ggwpggqgcqavemaledvnsrrdlpdyelk 211
 QY 82 LHSNDSECEPGLGASVMYNNLLNPKOKLMLLAGCSTVCTTVAEAAKMNLLVLCVGASSP 141
 DB 212 lihdskdqpgqatkylyellyndpikilmpgcsvsstlvaearmnnllvlsygsasp 271
 QY 142 ALSDRKREPTLFRTHPSATVHNPTRIKLMKFGNSRVAILQQAEEVFISTVEDLENRCME 201
 DB 272 alsnrqrftfrthpsatlhnptrvkifekwgwkkiatiqqtetvftldldeerveke 331
 QY 202 AGVEIVTRQSFLSDPTDAVRNLRRODARIIVGLFVVAARRVLCMEYKQOLYGRAHVWFF 261
 DB 332 agieitfrqsfdsdpavpvknkqrqdarilvglyfetearkvfcveykkyvfwf1 391
 QY 262 IGWYEDNWEYNLKAEGITCTVEQMRIAEGHLLTTEALMWNONNOTTSGMTAEERHRL 321
 DB 392 igwyadnwfk1--ydpstnctvdeanteaveghitcelvmlnpantrsnmscgefvekl 449
 QY 322 NQALIEGYDINHRYPE---GYQEAPLAYDAVSWALAFNAFNKMTBRLTTGKKSLRDTFT 378
 DB 450 tkrl-----krhpeetgfgaeplaydaialalalnktsgggsgvrldefnyn 500
 QY 379 DKEIADEIYAAMNSTQFLGVSGVAFSSQGDRIALTQTEQMDTGKYEKLYGTYDTQLDNLS 438
 DB 501 nqtitdqiyramnsssfegshvfvdasgrmawtllieqlggsgykykgyydstkddls 560
 QY 439 WLNEQWIGKGVPODRTIVTHVRLTVSLPLFVCMCTISCGIFVAFALIFINWKNHRV 498
 DB 561 wsktdkwlggppadqtlviktfrflsqflisvslsglglavvcflsnfynshvry 620
 QY 499 IQSSHPVCNTIMLFVCIILISVILLGIDGRFVSPDEEYPKICQARAWLLSTGFTLAYGAM 558
 DB 621 ignspnlnntavgcslalaavflgidghygnqrfvcqarllwllglfslgygsm 680
 QY 559 FSKVWRVHRFTTK--AKTDPKKKVEPKLYTMVWSGLLSIDLVLISWQTFDPLQRYLETF 616
 DB 681 ftklwwhtvftckeeekewrktlepkwkiyatvgilvgmdvltlailwqvdplhrtietf 740
 QY 617 PLEDPVSTTDDIKIRPELEHCSQNSMWLGVLGVGFKGLILVFLGFLAYETRSIKVKQIN 676
 DB 741 akeepkedi-dvsilpqlhecsskmtwlgfygkglililgflayetskvsstek 799
 QY 677 DSRVYVGSIIYVNVVLCLITAPVGMVIAQQDASFAFALAVIFCCFLSMLLIFVPKVIEV 736
 DB 800 dhravgmamynvavclitapvtmilsqqdaafafaalaivfssyiltvlvfpkmr1 859
 QY 737 IRHP--KDKAESKYNPDSAISKDEERYQKLVITENEQRLITQKEKIRVLQRBLVER 793
 DB 922 r 922

Db 860 itrgewqseqdtkmktgssnnneeksrllekenrelekiiaekeervselrhqlqsr 918

RESULT 10
AA28838
ID AAY28838 standard; Protein; 961 AA.
XX
AC AAY28838;
XX
DT 17-JAN-2000 (first entry)
DE Human GABABR1a receptor protein.
XX
KW GABABR1a receptor protein; cloning; rat brain; GABABR2; GABAB receptor;
KW human gamma-aminobutyric acid receptor; metabotropic receptor; screening;
KW synaptic transmission; GABABR1b; cloned receptor; splice variant;
KW modulatory agent; molecular activity assay; antispastic; anti-addictive;
KW antineurodegeneration; analgesic; cardiovascular activity.
OS Homo sapiens.
XX
PN WO9951636-A2.
XX
PD 14-OCT-1999.
XX
PF 02-APR-1999; 99WO-US07352.
XX
PR 03-APR-1998; 98US-0080676.
XX
PA (NPSF-) NPS PHARM INC.
PI Garrett JE, Simin RT, Busby JG, Stormann TM;
DR WPI; 1999-610994/52.
DR N-PSDB; AAX90920.
XX
PT Novel nucleic acids, used to screen for specific modulators, e.g. for
PT treating spasticity or Alzheimer's disease
PS Disclosure; Fig 2A-2F; 78pp; English.
XX
CC The present sequence is GABABR1a receptor protein cloned from rat brain.
CC This is closely related to GABABR2. GABAB receptors are metabotropic
CC receptors that modulate synaptic transmission in brain. GABABR1a differs
CC from GABABR1b in that the N-terminal 147 residues are replaced by 18
CC amino acids. Both of these cloned receptors appear to be splice variants.
CC They are expressed in cells that express GABABR2. They are used to raise
CC antibodies to screen for specific modulators. These modulators have
CC antispastic, antineurodegeneration, analgesic, anti-addictive,
CC cardiovascular activities.
XX
SQ Sequence 961 AA;

Query Match 46.4%; Score 2030.5; DB 20; Length 961;
Best Local Similarity 49.3%; Pred. No. 2.6e-192;
Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;

Qy 24 PHLQGVAGRPDE--LHIGGIPPIAGKGGWQGGQACMPATRLALDDVKNQPNLLPGFKLI 81
Db 155 phcqvnrtpshserravvialfpm--ggwpggacqcpavemaledvnsrdilpdyelk 212
Qy 82 LHSNDSECPGLGAVMYNLLYNKPKMLLAGCSNVTCTVAEAKMNLVLCYGASSP 141
Db 213 lhhdskdcpqgatkyllyellndpklilmpgcsstvtaeaaarmnlivisygssp 272
Qy 142 ALSDRKRPFTLFRTPSATVHNPTRIKMKKFGWSVAILQQAEEVFISTVEDLENRCME 201
Db 273 alsnrqrftftfrpsatlhnptrvklfekgwkkiaitqqtteftstldleerve 332
Qy 202 AGVEITVROSFTSDPTDAVNLRRQDARIIVGLFYVAARRVLCEMYKOOLYGRAHWFF 261
Db 333 agieitfqsfdsdpavpvknkrqdarliivgftearkvfcevykerlfgkkywfl 392

Qy 262 IGWYEDNNYEVNLRKAGITCTVEQMRIAEGHLLTTEALMWNQNNQTTISGMTAEERHRL 321
Db 393 igwyadnwfk--ydpnsinctvdmteaveghitfeivmlnpantrslsnmtsgefevki 450
Qy 322 NOALIEEGYDINHRYPE---CYQEAPLAYDAVWSVALAFNFKTMERLTTGKSLRDFTYT 378
Db 451 tkrl-----krhpeetggfqaepaladaiwalalalnlktsggggrsvrledfyn 501
Qy 379 DKETADEIYAAMNSTQFLGVSGVAFSSQGDRIATQIEMIDGKYEKLYGYDTOLDNIS 438
Db 502 nqtitdqiyramnsssfegvghvfdasgrmawtllieqlgggskkigydstkdlls 561
Qy 439 WLNTFQWIGGVQDRTIVTHVLRVSLPLFVCMCTISSCGIFVAFALLIFNIWKKHRY 498
Db 562 wsktdkwiggppadqtiwikfrlsqklfsvslslglvavvcisfnlyshvry 621
Qy 499 IQSSHPVCNTMLFCVITCLISVILLGIDGRFVSPPEYKICQARAWLLSTGFTLAYGAM 558
Db 622 iqnsqpnlnhtavgcslaaavfpldgynqrfvqcqarlwlglgfslygysm 681
Qy 559 FSKVVRVHRFTTK--AKTDPKKKVPKLYTMVSGLLSIDLVLLSWQIFDPLQRYLETF 616
Db 682 ftkiwwhtvftkkekewrktlepklyatvgllvgmdvltlaiwqivdplhrtietf 741
Qy 617 PLEDPVSTDDIKIRPELEHESQRNSMMLGLVYGFKLILVFLGFLAYETRSIKVKQIN 676
Db 742 akepkedi-dvslilpqlchcsrrkmtwlgifykglllllglflayetskstekln 800
Qy 677 DSRVGMISYVNVVLCILITAPVGMVIAQODASFALVAFVFCFSLMLLIVPKVIEV 736
Db 801 dhravgmalynvavllclitapvmlssqgdaafasialvissyitvllvfpkmrri 860
Qy 737 IRHP--KDKAESKNPDSAIKSEDEERYQKLVTEQQLRQITQKEEKIRVLQRIVER 793
Db 861 itrgewqseqdtkmktgssnnneeksrllekenrelekiiaekeervselrhqlqsr 919

RESULT 11
AA29798
ID AAY29798 standard; Protein; 961 AA.
XX
AC AAY29798;
XX
DT 15-NOV-1999 (first entry)
XX
DE Human gamma-amino-butyric acid B receptor subunit GABABR1a.
KW Gamma-amino-butyric acid B receptor subunit; HC20; GABABR1a;
KW depression; epilepsy; neuropsychiatric disorder; dementia;
KW muscular contraction; central nervous system disorder.
XX
OS Homo sapiens.
XX
PN WO9940114-A1.
XX
PD 12-AUG-1999.
XX
PF 03-FEB-1999; 99WO-US02361.
XX
PR 05-FEB-1998; 98US-0073767.
XX
PA (MERI) MERCK & CO INC.
PA (MERI) MERCK FROSST CANADA INC.
PA (JYTE-) UNIV TEXAS HEALTH SCI CENT SAN ANTONI.
PA (USSH) US NAT INST OF HEALTH.
XX
PI Bonner TJ, Bonner TP, Clark J, Kolakowski LF, Liu Q;
PI McDonald T, Ng GY;
XX
DR WPI; 1999-527300/44.
DR N-PSDB; AAZ06970.
XX

PT New DNA encoding human and murine receptor subunits, useful for
PT identifying agonists and antagonists for treatment of depression,
XX epilepsy and neuropsychiatric disorders
XX
XX
XX Claim 11; Fig 18; 128pp; English.

CC The present sequence represents a human gamma-amino-butyric acid (GABA)
CC B receptor (GABAR) subunit designated GABABR1A. The present invention
CC also describes the GABAR subunit designated HG20. Cells expressing
CC the new receptor subunits are useful for identifying GABAR agonists
CC and antagonists. HG20 proteins and their antagonists are useful for
CC inhibiting HG20 or GABAR function, useful for treating depression,
CC epilepsy, neuropsychiatric disorders, dementias, muscular contractions,
CC and central nervous system disorders.

XX
SQ Sequence 961 AA;

Query Match 46.4%; Score 2030.5; DB 20; Length 961;
Best Local Similarity 49.3%; Pred. No. 2.6e-192;
Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;

QY 24 PHLOGVAGRPDE--LHIGGIFPIAGKGGQACMPATRLALDDVKNPOLLPGFKLI 81
DB 155 phcqvrtphserravvigaifpms--ggwpggacqapavemaledvnsrrdlpdyelk 212
QY 82 LHSNDECEPGLGASVYNNLYNKPQKMLLAGCSTVCTTVAEAAKMWNLIVLCYGASSP 141
DB 213 lihdsckdpggatkyllyellyndpikilmpgcssvstlvaaearmwnlivlysgssp 272
QY 142 ALSDRKRPTLFRTHPSATVHNPTRIKMKFGWSRVAILQQAEEVFISTVEDLENRCME 201
DB 273 alsnrgfrptftrhpsatlhnptrvklfekwggkktiatiqgttevtstlddleervke 332
QY 202 AGVEIVTROSEFLSDPTDAVNLRRODRIIVGLFVVAARRVLCMVKQOOLYGRAHWYFF 261
DB 333 agieifrfgsdpavpvnkrlqdarliivfyetearkvcevykerlfgkkywfl 392
QY 262 IGWYEDNWTEVNLKAEICTVEQMRTIAEAGHLTTEALMNNQNTTISGMTAEFRHRL 321
DB 393 igwyadnwfkii--ydpisinctvdeaveghittelvmlnpantrsisnmtsqefvekl 450
QY 322 NQALIEEGYDINDRPE---GEOEAPLAYDAVMSVALAFNKNWERTLTGKKSRLDFTYT 378
DB 451 tkrl-----krhpeetggfgeaplaydaiwalalanktsgggrsvrlednyn 501
QY 379 DKEIADIEIYAAMNSTOPLGVSGVVAESOGDRIALTOEIMDKYKELGYDPTQDLNLS 438
DB 502 nqitqdiyramnssfgsvghvfdasgsrmaawtlieqlggysykgigydstkdolis 561
QY 439 WLNTQEWIGKVPQDRITIVHVLRTVSLPLFVCMCTISSGIFVAFALIIFNWKNHRRV 498
DB 562 wsktdkwgspadqtlvktfrlsqkifsvsvlssgvlavclslfniynshvry 621
QY 499 IQSSHPVCNTIMPLGVIIICILISVILLIDGRFVSPPEYKICQARAWLLSGFTLAYGAM 558
DB 622 iqsqpnlnltaavgcsalaaavfplglgdyhigrndpfvcqarlwlglgslgygsm 681
QY 559 FSKVWRVHRETTK--AKTDPKKVPEPKWLTVMVSGLLSIDVLVLLSQIFDPLORYLETF 616
DB 682 ftklwwhtvftkeekewrktlepklyatvgllvlgmdvltalwqivdpplrhtetf 741
QY 617 PLEDVPTSTDDIKIRPLEHCESSORNSMWLGLVYFGKGLIIVFLGFLAYEPRSKVKQIN 676
DB 742 akeepkedl-dvslpqlehcscrkmtwlgifygkglllgliflayecksvstekin 800
QY 677 DSRVYGMISYNNVVLICLTAPVGMVITASQODASFAFVALVAFCCFLSMILLIFVPKVEV 736
DB 801 dhravgmaiynvavclitapvtmilssqdaafafaslaivfssytlvlvfpkmrll 860
QY 737 IRHP--KDAESKYNPDSAISKDEERYQKLVTEENQOLRITOKEKIRVLRORLVER 793
DB 861 itrgewgseqdtkmgtsgstnnneeksrillekenreleliaekeervslrhlqsr 919

RESULT 12

AAAY14101
ID AAY14101 standard; Protein; 961 AA.

XX
XX AAY14101;

AC AAY14101;

XX 21-JUL-1999 (first entry)

XX Human GABAB receptor 1a protein sequence.

XX GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;
KW transient lower oesophageal sphincter relaxation; spasticity; emesis;
KW gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;
KW irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;
KW autoimmune disease; neoplastic disease; infectious disease; therapy.

XX Homo sapiens.

OS WO9921890-A1.

XX 06-MAY-1999.

XX 27-OCT-1998; 98WO-SE01947.

XX 17-JUL-1998; 98SE-0002575.

XX 27-OCT-1997; 97SE-0003914.

XX 16-MAR-1998; 98SE-0000864.

XX (ASTR) ASTRA AB.

XX Ekstrand J;

XX WPI: 1999-302985/25.

XX N-PSDB; AAX58054.

PT Polynucleotides encoding human and canine gamma aminobutyric acid
PT type B receptors, used to screen for compounds that are inhibitors
PT of transient lower oesophageal sphincter relaxations

XX Claim 17; Page 79-84; 222pp; English.

CC This sequence is a human gamma aminobutyric acid type B (GABAB)
CC receptor of the invention. Nucleic acid molecules encoding GABAB
CC receptors can be used to screen for compounds that are inhibitors of
CC transient lower oesophageal sphincter relaxations (TLESR). They can also
CC be used to screen for agonists or antagonists of the GABAB receptors.
CC Inhibitors of TLESR are useful for treating gastro-oesophageal reflux
CC disease. Other uses of GABAB receptors, such as human GABAB R1c or 1d,
CC comprise diagnosis or treatment of conditions related to GABAB
CC dysfunction, e.g. epilepsy, psychiatric disorders, emesis, irritable
CC bowel syndrome, dyspepsia, spasticity, arthritis, allergies, autoimmune
CC diseases, neoplastic diseases, pain and infectious disease.

XX Sequence 961 AA;

Query Match 46.4%; Score 2030.5; DB 20; Length 961;
Best Local Similarity 49.3%; Pred. No. 2.6e-192;
Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;

QY 24 PHLOGVAGRPDE--LHIGGIFPIAGKGGQACMPATRLALDDVKNPOLLPGFKLI 81

DB 155 phcqvrtphserravvigaifpms--ggwpggacqapavemaledvnsrrdlpdyelk 212

QY 82 LHSNDECEPGLGASVYNNLYNKPQKMLLAGCSTVCTTVAEAAKMWNLIVLCYGASSP 141

DB 213 lihdsckdpggatkyllyellyndpikilmpgcssvstlvaaearmwnlivlysgssp 272

QY 142 ALSDRKRPTLFRTHPSATVHNPTRIKMKFGWSRVAILQQAEEVFISTVEDLENRCME 201

DB 273 alsnrgfrptftrhpsatlhnptrvklfekwggkktiatiqgttevtstlddleervke 332

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QY 202 AGVEITVROSFLSDPTDAVNRLLRQDARIIVGLFVVAARRVLCEMYKQOOLYGRAHWVFF 261
Db 333 agieitfrsffsdapvpvknkrqdarilvgifetearkvfcevykerlfgkkywfl 392
QY 262 IGWYEDNMYEVLNKGAGITCTVEQMRIAAGHLTTEALMNNQNTTISGMTAEFRHRL 321
Db 393 igwyadnwfk--ydpisinctvdeatveghitteivmlpantrtsismtsqefvkl 450
QY 322 NQALIEEGYDINHRYPE---GYQEAFLAYDAVWSVALAFNKTMRERLTGKKSRLDRFTYT 378
Db 451 tkrl-----krhpeetggfqaepaydaiwalalalnktsksggrsvrledfyn 501
QY 379 DKEIADEIYAAMNSTQFLGSGVAVFSSQGDRIALTQEQMDGKYELGYDTOLDNLS 438
Db 502 nqtitdqiyranssssfegsvghvfdasgrmawtlieqlggsykkigydstkddls 561
QY 439 WLNTEQWIGKVPQDRTIVTHVLRVSLPLFVCMCTISSCGIFVAFALIIFNIWKNHRRV 498
Db 562 wsktdkwigspadqtlviktfrfsqklfisvslsllgvlavvclsfniynshvry 621
QY 499 IQSSHVPVCNTIMLFGVILCLISVILLIDGRFVSPBEYPKICQARAWLLSTGFTLAYGAM 558
Db 622 iqnsqpnlnltavgsalaaavfplgdghyhgrrnqpfvcqarlwlglgfslygsm 681
QY 559 FSKVHRVHRTTK--AKTDPKKVPEWKLTYMTWSGLSIDLVILLSHQIFDPLQRYLETF 616
Db 682 ftkiwwhvtfckkeekewrklepklyatvgllvgmdvltlaiwqivdphtletf 741
QY 617 PLEDPVSTTDDIKIRPELEHESQORSNMLGVYGFKGLILVGLFLAYETRSFKVKQIN 676
Db 742 akeepedi-dvsilpqlehcscrsmntwlgifygkglillilgflayeksvstekin 800
QY 677 DSRVYGMSTYVNVVLCITAPVGMVIAQQDASFAFVALAVIFCCFLSMLLIFFPKVIEV 736
Db 801 dhraqvmaynvavclitapvtmilssqqdaafastaivfssyitlvlfvpmrri 860
QY 737 IRHP--KDKAESKYNPDSAISKEDEERYOKLVNTENQOLRLITQKEKIRVLQRVER 793
Db 861 itrgevwseqadtmtkgsntnnneeksrllekenrelekiiaekeervseltrhqlqsr 919

RESULT 13
AA49133
ID AA49133 standard; Protein; 1323 AA.
AC AA49133;
XX
DT 07-JAN-2000 (first entry)
DE
DE GABA-BR1a*Gqo5 fusion construct protein sequence.
XX
KW G-protein fusion receptor; CaR; calcium receptor; GluR; head injury;
KW metabotropic glutamate receptor; GABAR; chimeric receptor; stroke;
KW gamma-aminobutyric acid receptor; allosteric modulator; anoxia;
KW spinal cord injury; epilepsy; ischaemia; hypoglycaemia; anoxia;
KW Alzheimer's disease; hyperparathyroidism; osteoporosis; depression;
KW cognitive disorder.
XX
OS Homo sapiens.
XX
PN W0951641-A1.
XX
PD 14-OCT-1999.
XX
PF 02-APR-1999; 98WO-0507333.
XX
PR 03-APR-1998; 98US-0080671.
XX
PA (NPS- ) NPS PHARM INC.
XX
PI Stormann TM, Hammerland LG, Storjohann LL, Busby JG, Garrett JE,
PI Simin RT;
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XX WPI: 1999-610995/52.
DR N-PSDB; AAZ31064.
XX
PT New G-protein fusion receptors and chimeras containing domains from
PT different receptors, used to screen for modulators, potentially useful
PT e.g. for treating or preventing stroke or Alzheimer's disease -
XX
XX Disclosure; Fig 14; 255pp; English.
XX
CC The invention relates to G-protein fusion receptors (I) comprising:
CC (1) in the N to C direction, extracellular (ECD), transmembrane (TMD) and
CC intracellular (ICD) domains, each chosen independently from a CaR
CC (calcium receptor), GluR (metabotropic glutamate receptor) and GABAR
CC (gamma-aminobutyric acid receptor); (2) an optional linker attached to
CC the C-terminus of ICD; and (3) a G-protein (GP) linked to ICD or the GP
CC linker. (I), and recombinant chimeric receptors (CR) without the GP
CC component, are used to assess function of the various domains and to
CC identify compounds (e.g. allosteric modulators or antagonists) that act
CC on these domains. The modulators are potentially useful for treating or
CC preventing diseases associated with the receptors, e.g. stroke, head or
CC spinal cord injury, epilepsy, ischaemia, hypoglycaemia, anoxia,
CC Alzheimer's disease, hyperparathyroidism, osteoporosis, cognitive
CC disorders and depression. Nucleic acid (II) that encodes (I) is used:
CC (1) for recombinant production of corresponding proteins; and (2) to
CC produce cells used in screening for modulators. Use of CaR and mGluR
CC domains allows presentation of GABAR domains, to a binding agent, in a
CC form more like the natural domain structure compared with use of
CC incomplete receptors, lacking one or more domains. By shuffling different
CC domains, agents can be identified that affect particular domains of a
CC receptor.
XX
SQ Sequence 1323 AA;
Query Match 46.4%; Score 2030.5; DB 20; Length 1323;
Best Local Similarity 49.3%; Pred. No. 4.4e-192;
Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;
QY 24 PHLOGGVAGRDE--LHTGGIFPTIAGKGGOGQACMPATRLALDDVKNQPNLPGFKLI 81
Db 155 phcvnrtpsherravvlgalfpms--ggwpggqacqpavemaledvnsrdilpdyelk 212
QY 82 LHSNDSCEPGLGASVMYNLLYNKPQKLMLLAGCSTVCTTVAEAAKMWNLIIVCYGASSP 141
Db 213 lihdsckdpggatkyllyellyndpikilmpgcsvstlvaearmwnliivlysgsssp 272
QY 142 ALSDRKRPTLFRTHPSATVHNTPRIKMKKPGWSRVAILQQAEEVFISTVEDLENRCME 201
Db 273 alsnrqrfptfrthpsatlhnptrvklifekgwkkiatqqttevfstidddleervke 332
QY 202 AGVEITVROSFLSDPTDAVNRLLRQDARIIVGLFVVAARRVLCEMYKQOOLYGRAHWVFF 261
Db 333 agieitfrsffsdapvpvknkrqdarilvgifetearkvfcevykerlfgkkywfl 392
QY 262 IGWYEDNMYEVLNKGAGITCTVEQMRIAAGHLTTEALMNNQNTTISGMTAEFRHRL 321
Db 393 igwyadnwfk--ydpisinctvdeatveghitteivmlpantrtsismtsqefvkl 450
QY 322 NQALIEEGYDINHRYPE---GYQEAFLAYDAVWSVALAFNKTMRERLTGKKSRLDRFTYT 378
Db 451 tkrl-----krhpeetggfqaepaydaiwalalalnktsksggrsvrledfyn 501
QY 379 DKEIADEIYAAMNSTQFLGSGVAVFSSQGDRIALTQEQMDGKYELGYDTOLDNLS 438
Db 502 nqtitdqiyranssssfegsvghvfdasgrmawtlieqlggsykkigydstkddls 561
QY 439 WLNTEQWIGKVPQDRTIVTHVLRVSLPLFVCMCTISSCGIFVAFALIIFNIWKNHRRV 498
Db 562 wsktdkwigspadqtlviktfrfsqklfisvslsllgvlavvclsfniynshvry 621
QY 499 IQSSHVPVCNTIMLFGVILCLISVILLIDGRFVSPBEYPKICQARAWLLSTGFTLAYGAM 558
Db 622 iqnsqpnlnltavgsalaaavfplgdghyhgrrnqpfvcqarlwlglgfslygsm 681
QY 559 FSKVHRVHRTTK--AKTDPKKVPEWKLTYMTWSGLSIDLVILLSHQIFDPLQRYLETF 616
Db 682 ftkiwwhvtfckkeekewrklepklyatvgllvgmdvltlaiwqivdphtletf 741
QY 617 PLEDPVSTTDDIKIRPELEHESQORSNMLGVYGFKGLILVGLFLAYETRSFKVKQIN 676
Db 742 akeepedi-dvsilpqlehcscrsmntwlgifygkglillilgflayeksvstekin 800
QY 677 DSRVYGMSTYVNVVLCITAPVGMVIAQQDASFAFVALAVIFCCFLSMLLIFFPKVIEV 736
Db 801 dhraqvmaynvavclitapvtmilssqqdaafastaivfssyitlvlfvpmrri 860
QY 737 IRHP--KDKAESKYNPDSAISKEDEERYOKLVNTENQOLRLITQKEKIRVLQRVER 793
Db 861 itrgevwseqadtmtkgsntnnneeksrllekenrelekiiaekeervseltrhqlqsr 919
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Db 622 iqnsqpnlnltavgcslalaavfplgldgyhigrnqfpvcqarlwlglgfslygysm 681
QY 559 FSKVWRVHRTTK--AKTDPKKKVPEWKLYTMVSGLLSIDIVLLSQIFDPLQRYLETF 616
Db 682 ftklwwhtvftkkekewrktlepklyatvgllvgmdvltaiwqivdplhrtietf 741
QY 617 PLEDVSTTDDIKTRPELEHCEORNWGLVYGFGLIILVFLGFLAYETRSKVKOIN 676
Db 742 akeepedi-dvsilpqlencssrkmtwifgygklllglflayeksvstekin 800
QY 677 DSRVYGMSIYNVWVLCITAPVGMVIAOODASFAFVALAVIFCCFLSMLLIFVPKVIET 736
Db 801 dhravgmaynvavclitapvtmilssqdaafafaslaivfssyiclvifvpkmrri 860
QY 737 IRHP--KDKAESKNPDASKEDEERYQKLVTENEQLRLITQKEEKIRVLRLQRLVER 793
Db 861 itrgewqseqdmtkgtsgstnnneeksrllikenrelekiakkeervselrhqlqsr 919

RESULT 14
AAW40117
ID AAW40117 standard; Protein; 793 AA.
XX
AC AAW40117;
XX
DT 03-JUN-1998 (first entry)
XX
DE Human GABA-BR1a/b receptor protein.
XX
KW Gamma-aminobutyric acid; GABA-BR1a/b receptor; human; brain; agonist;
KW inhibitory neurotransmitter; peripheral nervous system; antagonist;
KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
KW epilepsy; cognitive function.
XX
OS Homo sapiens.
XX
PN WO9746675-A1.
XX
PD 11-DEC-1997.
XX
PF 19-MAR-1997; 97WO-EP01370.
XX
PR 22-NOV-1996; 96US-0756091.
PR 30-MAY-1996; 96US-0655716.
XX
PA (NOVS ) NOVARTIS AG.
XX
PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;
XX
DR WPI; 1998-042183/04.
DR N-PSDB; AAV10265.
XX
PT Purified GABA-B receptor or receptor protein - and antagonists of
PT these which may be useful in treating nervous system disorders
XX
PS Claim 4; Page 62-67; 108pp; English.
XX
CC This sequence represents a novel human GABA-B receptor protein,
CC GABA-BR1a/b. GABA (gamma-aminobutyric acid) is the major inhibitory
CC neurotransmitter found in the brain and peripheral nervous system
CC and this receptor may be used for the identification of GABA-B
CC receptor agonists and antagonists. Such proteins may be used in
CC treatment of dementia, depression, anxiety, epilepsy, spasticity,
CC bronchial inflammation or asthma or to improve cognitive function.
CC GABA-B receptor ligands and probes derived from this sequence can be
CC used to assay for GABA-B receptors or DNA encoding them.
XX
SQ Sequence 793 AA;

Query Match 46.4%; Score 2029.5; DB 19; Length 793;
Best Local Similarity 49.9%; Pred. No. 2.4e-192;
Matches 381; Conservative 151; Mismatches 211; Indels 21; Gaps 7;

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QY 37 LHIGIFPIAGKGWGGQACMPATRLALDDVKNQPNLLPGFKLILHSNDSCEPGLGAS 96
Db 2 vyigalfpms--ggwpgggacpavemaledvnsrrdilpdyelkllhdsdcdpgatk 59
QY 97 VMYNLLYKPKQLMALLAGCSTVCTTVAEAAKWNLLIVLCYGASSPALSBRKRPFTLFRTH 156
Db 60 yiyellyndpikilimpccssvstlvaearmnlivlsygsppalsnqrqfptfrth 119
QY 157 PSATVHNPTRIKLMKFGMSRVAIIQQOAEVFISTVEDLENRCMEAGVELTVRQSLSDP 216
Db 120 psathhnptrvlfekwggkktiatqqttevftstldleerkeagietfrqsfssdp 179
QY 217 TDVARNLRQDARIIVGLFVYVAARVLCMEYKQQLYGRAHVFYFFGWEDNMWYNLKA 276
Db 180 avpvnlkrqdarilvlfeyetearkvfcevkykerlfgkkyvflwgadnwfkli--yd 237
QY 277 EGITCTVEOMRTAAEGHLTTEALMWNQNNQTTISGMTAEFRHLRNLQALIEBEGYDINHDR 336
Db 238 psinctvdeataveghitteivmnpntrsisnmtsqefvekltrli-----kr 288
QY 337 YPE--GYQEAPLAYDAVMSVALAFNKTMERLTTGKKSRLRDTYTDKEADEIYAAANST 393
Db 289 npeetggfgeaplaydaivalalanktsggggrsvrlfedfnynnqtltdqlyramns 348
QY 394 QFLGVSGVYAFSSQGDRIALTQIEQIDGKYBKLYGYYDTQDLNLSWLNTEQWIGKVPQD 453
Db 349 sfegvsgvhvfdasgsrmawtlieqlggsgykyggydstkdlswsktdkwiggspad 408
QY 454 RTIVTHVLRTVSLPFCVMCTTSSCGIFVAFALIIIFNINWKNHRRVITQSSHPVCNTIMLFG 513
Db 409 qllviktfrfslsqkifisvsvlssigivlavvclslfniynshvryiqnsqpnlnltavg 468
QY 514 VTICLISVLLGIDGRFVSPEEPYKICQARAWLLSGFTLAYCAMEFSKVRVHRFTTK-- 571
Db 469 csialaavfplgldgyhigrnqfpvcqarlwlglgfslygysmtkikiwwhtvftkke 528
QY 572 AKTDPKKKVPEWKLYTMVSGLLSIDIVLLSQIFDPLQRYLETFPLEPVPSTDDIKIR 631
Db 529 ekewrktlepklyatvgllvgmdvltaiwqivdplhrtietakeepedi-dvsil 587
QY 632 PELEHCEORNWGLVYGFGLIILVFLGFLAYETRSIKVKOINSDRSYVMSIYNVWL 691
Db 588 pqlchcssrkmtwifgygklllglflayeksvstekindhravgmaynvavl 647
QY 692 CLITAPVGMVIAOODASFAFVALAVIFCCFLSMLLIFVPKVIETIRHP--KDKAESKN 749
Db 648 clitapvtmilssqdaafafaslaivfssyitlvifvpkmrriitrgewqseqdmtk 707
QY 750 PDSAISKEDEERYQKLVTENEQLRLITQKEEKIRVLRLQRLVER 793
Db 708 tgsstnnneeksrllikenrelekiakkeervselrhqlqsr 751

RESULT 15
AAV14109
ID AAV14109 standard; Protein; 892 AA.
XX
AC AAV14109;
XX
DT 21-JUL-1999 (first entry)
XX
DE Human GABAB receptor 1g protein sequence.
XX
KW GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;
KW transient lower oesophageal sphincter relaxation; spasticity; emesis;
KW gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;
KW irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;
KW autoimmune disease; neoplastic disease; infectious disease; therapy;
KW alternative splicing; isoform.
XX
OS Homo sapiens.
XX

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